

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 18:52:59 ; Search time 75.2941 Seconds
(without alignments)
58.355 Million cell updates/sec

Title: US-09-529-206E-15
Perfect score: 47
Sequence: 1 TVSGNLTIR 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	10	2	AAY05980 Human can
2	47	100.0	10	2	AAY05988 Human can
3	47	100.0	14	4	AAG07788 Human NY
4	47	100.0	14	4	AAG07728 Human NY
5	47	100.0	15	4	AAG07726 Human NY
6	47	100.0	15	4	AAG07727 Human NY
7	47	100.0	15	4	AAG07786 Human NY
8	47	100.0	15	4	AAG07787 Human NY
9	47	100.0	18	3	AAY52440 Human tum
10	47	100.0	18	4	AAB69940 Human NY
11	47	100.0	18	4	AAB69944 Human NY
12	47	100.0	18	4	AAU01544 Human NY
13	47	100.0	18	4	AAU01540 HLA-DR53
14	47	100.0	18	4	AAE07769 Human NY
15	47	100.0	18	9	ADW50855 NY-ESO-1
16	47	100.0	18	9	ADW50855 NY-ESO-1
17	47	100.0	20	4	ADW08648 Class II
18	47	100.0	20	4	AAG07742 Human ESO
19	47	100.0	20	8	AD119891 Human HLA
20	47	100.0	20	8	AD119048 Human HLA
21	47	100.0	20	8	ADJ58397 Peptide p
22	47	100.0	20	9	ADZ67819 Major his
23	47	100.0	25	4	AAG07718 Human NY
24	47	100.0	25	7	ADD71521 HLA-DP4 b
25	47	100.0	25	9	ADZ67810 Major his

25	47	100.0	27	4	AAE07717	Aae07717 Human NY
26	47	100.0	30	5	AAU85110	Aau85110 Human NYN
27	47	100.0	36	5	ABG79131	Abg79131 Human NY-
28	47	100.0	54	8	ADG89697	Adg89697 Class II
29	47	100.0	123	8	ADQ10452	Adq10452 Epitope 1
30	47	100.0	123	8	ADS80932	Ads80932 DNA plasm
31	47	100.0	179	8	ADK68648	Adk68648 Epitope 1
32	47	100.0	179	8	ADK68657	Adk68657 Epitope 1
33	47	100.0	179	8	ADQ10455	Adq10455 Epitope 1
34	47	100.0	179	8	ADS80935	Ads80935 DNA plasm
35	47	100.0	180	2	AAW62584	Aaw62584 Cancer as
36	47	100.0	180	2	AAW69865	Aaw69865 Human NY-
37	47	100.0	180	2	AAW52430	Aaw52430 Human can
38	47	100.0	180	3	AAW52430	Aaw52430 Human tum
39	47	100.0	180	3	AAW70862	Aaw70862 Human tum
40	47	100.0	180	3	AAW03154	Aaw03154 Human oes
41	47	100.0	180	4	AAW69946	Aaw69946 Human NY-
42	47	100.0	180	4	AAW67164	Aaw67164 Amino aci
43	47	100.0	180	4	AAU01535	Aau01535 Human NY-
44	47	100.0	180	4	AAE07714	Aae07714 Human NY
45	47	100.0	180	5	AAU84818	Aau84818 Human NYN

ALIGNMENTS

RESULT 1

AA05980

ID AAY05980 standard; peptide; 10 AA.

XX

AC AAY05980;

XX

DT 16-AUG-1999 (first entry)

XX

DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide ESO10-127.

XX

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;

KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;

KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;

KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;

KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;

KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;

KW vaccine.

XX

OS Homo sapiens.

XX

PN WO9918206-A2.

XX

PD 15-APR-1999.

XX

PF 21-SEP-1998; 98WO-US019609.

XX

PR 08-OCT-1997; 97US-0061428P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Wang RF, Rosenberg SA;

XX

DR WPI; 1999-277270/23.

XX

PT Cancer antigen NY ESO1/CAG-3.

XX

PS Claim 17; Page 64; 88pp; English.

XX

CC This sequence represents cancer peptide ESO10-127 that corresponds to

CC amino acid residues 127-136 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see

CC AAY05965), a new and potent tumour antigen capable of eliciting an

CC antigen specific immune response by T cells. Cancer peptides derived from

CC CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their

CC variants (see AAY05967-87), are useful as cancer vaccines that protect

CC against cancer. The invention provides: vectors and host cells (also

CC useful as vaccines); a method of diagnosis of cancer or precancer; a

CC transgenic animal; antisense oligonucleotides that inhibit expression of

CC the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
 CC cancer peptide, useful in diagnostic and detection assays; and methods
 CC for preventing or inhibiting cancer by administering a cancer peptide,
 CC with or without an HLA molecule. The cancer peptides form part of, or are
 CC derived from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
 CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
 CC treated by inducing cancer-specific T cells in vitro for subsequent
 CC return to a patient

XX Sequence 10 AA;

Query Match 100.0%; Score 47; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.004;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 |||||
 DB 1 TVSGNLTIR 10

RESULT 2

AA05988
 ID AAY05988 standard; peptide; 10 AA.

XX AAY05988;

AC AAY05988;

CT 16-AUG-1999 (first entry)

DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine; human leukocyte antigen; HLA.

OS Homo sapiens.

XX WO9918206-A2.

PN 15-APR-1999.

XX 21-SEP-1998; 98WO-US019609.

XX 08-OCT-1997; 97US-0061428P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang RF, Rosenberg SA;

XX WPI; 1999-277270/23.

XX Cancer antigen NY ESO1/CAG-3.

XX Example 10; Page 42; 88pp; English.

XX This peptide was identified as an HLA peptide motif following a screen
 CC for epitopes from the coding region of human NY ESO-1/CAG-3 ORF1 (see
 CC AX58599). 30 Epitopes (see AAY05988-Y06017) were identified. The present
 CC peptide (ranked 1) corresponds to amino acid residues 127-136 of CAG-1
 CC ORF1 (see AAY05965). CAG-1 is a new and potent tumour antigen capable of
 CC eliciting an antigen specific immune response by T cells. Cancer peptides
 CC (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their
 CC variants, are useful as cancer vaccines. A claimed method of preventing
 CC or inhibiting cancer involves administering a cancer peptide, with or
 CC without an HLA molecule. The cancer peptides form part of, or are derived
 CC from, cancers such as primary or metastatic melanoma, thymoma, lymphoma,
 CC sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
 CC cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,

CC prostate, ovarian, pancreatic and thyroid cancers

XX Sequence 10 AA;

Query Match 100.0%; Score 47; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.004;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 |||||
 DB 1 TVSGNLTIR 10

RESULT 3

AAE07788
 ID AAE07788 standard; peptide; 14 AA.

XX AAE07788;

XX 06-NOV-2001 (first entry)

DE Human NY ESO-1 peptide #22 to characterise epitope recognised by TE4-1.

XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
 KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 KW NY ESO-1 protein; CD4+ T lymphocyte; human leukocyte antigen; HLA;
 KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
 KW immunotherapy.

OS Homo sapiens.

XX WO200155393-A2.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US002765.

XX 28-JAN-2000; 2000US-0179004P.

XX 29-SEP-2000; 2000US-0237107P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang R, Rosenberg SA, Zeng G;

XX WPI; 2001-496851/54.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 CC useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 CC protection from metastasis.

XX Example 6; Fig 6A; 134pp; English.

XX The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leukocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any given
 CC target antigen and/or haptan and to induce tumour-specific humoral-
 CC mediated immunity against cancer. The present sequence is human NY ESO-1
 CC peptide used in the characterisation of the NY ESO-1 epitope recognised
 CC by TE4-1

XX Sequence 14 AA;

XX SQ

Query Match 100.0%; Score 47; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TVSGNLTIR 10
 DB 4 TVSGNLTIR 13

RESULT 4
 AAE07728
 ID AAE07728 standard; peptide; 14 AA.
 XX AC AAE07728;

06-NOV-2001 (first entry)
 Human NY ESO-1 MHC class II restricted T cell epitope #14.

Human; major histocompatibility complex; MHC; vaccine; metastasis;
 class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 tumour-specific humoral-mediated immunity; cancer; cytostatic;
 immunotherapy.

OS Homo sapiens.
 XX WO200155393-A2.
 XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US002765.
 XX 28-JAN-2000; 2000US-0179004P.
 XX 29-SEP-2000; 2000US-0237107P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang R, Rosenberg SA, Zeng G;
 XX WPI; 2001-496851/54.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis.

XX Claim 4; Page 16; 134pp; English.

XX The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any given
 CC target antigen and/or haptens and to induce tumour-specific humoral-
 CC mediated immunity against cancer. The present sequence is MHC class II
 CC restricted T cell epitope of human NY ESO-1 protein

XX Sequence 14 AA;

Query Match 100.0%; Score 47; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TVSGNLTIR 10

DB 4 TVSGNLTIR 13

RESULT 5
 AAE07726
 ID AAE07726 standard; peptide; 15 AA.
 XX AC AAE07726;

06-NOV-2001 (first entry)

Human NY ESO-1 MHC class II restricted T cell epitope #12.

Human; major histocompatibility complex; MHC; vaccine; metastasis;
 class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 tumour-specific humoral-mediated immunity; cancer; cytostatic;
 immunotherapy.

OS Homo sapiens.
 XX WO200155393-A2.
 XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US002765.
 XX 28-JAN-2000; 2000US-0179004P.
 XX 29-SEP-2000; 2000US-0237107P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang R, Rosenberg SA, Zeng G;
 XX WPI; 2001-496851/54.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis.

XX Claim 4; Page 16; 134pp; English.

XX The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any given
 CC target antigen and/or haptens and to induce tumour-specific humoral-
 CC mediated immunity against cancer. The present sequence is MHC class II
 CC restricted T cell epitope of human NY ESO-1 protein

XX Sequence 15 AA;

Query Match 100.0%; Score 47; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0067;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TVSGNLTIR 10
 DB 6 TVSGNLTIR 15

RESULT 6

RESULT 7
AAE07786
ID AAE07786 standard; peptide; 15 AA.

KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
 KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 KW NY ESO-1 protein; CD4+ T lymphocyte; human leukocyte antigen; HLA;
 KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
 KW immunotherapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200155393-A2..
 XX
 PD 02-AUG-2001.
 XX
 PF 26-JAN-2001; 2001WO-US002765.
 XX
 XX 28-JAN-2000; 2000US-0179004P.
 PR 29-SEP-2000; 2000US-0237107P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Wang R, Rosenberg SA, Zeng G;
 XX WPI; 2001-496851/54.
 DR
 XX
 XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis.
 PT
 XX Example 6; Fig 6A; 134pp; English.
 PS
 XX The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leukocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any given
 CC target antigen and/or hapten and to induce tumour-specific humoral-
 CC mediated immunity against cancer. The present sequence is human NY ESO-1
 CC peptide used in the characterisation of the NY ESO-1 epitope recognised
 CC by TB4-1
 XX
 XX Sequence 15 AA;
 SQ

Query Match 100.0%; Score 47; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0067;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 |||||
 DB 5 TVSGNLTIR 14

RESULT 9
 AAY52440
 ID AAY52440 standard; protein; 18 AA.
 XX
 AC AAY52440;
 XX
 DT 15-FEB-2000 (first entry)
 XX
 DE Human tumour antigen NY-ESO-1 peptide #13.
 XX
 KW Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;
 KW T-cell; helper; stimulation; proliferation; treatment; diagnosis;
 KW prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;
 KW hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.

XX Synthetic.
 OS Homo sapiens.
 XX
 PN WO9953938-A1.
 XX
 XX 28-OCT-1999.
 XX
 XX 24-MAR-1999; 99WO-US006875.
 PF
 XX 17-APR-1998; 98US-00062422.
 PR 02-OCT-1998; 98US-00165546.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
 PI Gure A, Ritter G;
 XX
 XX WPI; 2000-038483/03.
 DR
 XX
 XX Novel peptides which bind to MHC class I and MHC class II molecules,
 PT useful for therapeutic and diagnostic purposes.
 PT
 XX Claim 4; Page 22; 49pp; English.
 PS
 XX Peptides #8-#13 (AAY52435-Y52440) are peptides derived from the human
 CC tumour antigen, NY-ESO-1 (AAY52430) which can bind to MHC(major
 CC histocompatibility Class II HLA-DR53 molecules, thereby stimulating
 CC proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially
 CC isolated from an oesophagus squamous cell cancer cDNA library. Tissue
 CC localisation studies revealed it to be expressed at high levels in normal
 CC ovary and testis but not in normal colon, kidney, liver, brain,
 CC oesophagus and skin. It was expressed in certain tumours and tumour cell
 CC lines with some degree of frequency - these included melanoma specimens
 CC and cell lines, and breast and bladder cancer specimens, with expression
 CC in other tumour types being sporadic. These NY-ESO-1-derived peptides may
 CC be used in methods and compositions used for the treatment, diagnosis and
 CC prevention of cancers (such as melanoma, breast cancer, prostate cancer,
 CC lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or
 CC lymphoma) and to stimulate the proliferation of T cells
 XX
 XX Sequence 18 AA;
 SQ

Query Match 100.0%; Score 47; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.0084;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 |||||
 DB 1 TVSGNLTIR 10

RESULT 10
 AAB69940
 ID AAB69940 standard; peptide; 18 AA.
 XX
 AC AAB69940;
 XX
 DT 27-APR-2001 (first entry)
 XX
 DE Human NY-ESO-1 HLA-DR53 binding motif #2.
 XX
 KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
 KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
 KW non-small cell lung carcinoma; tumour status determination.
 XX
 XX Homo sapiens.
 OS
 XX WO200107917-A1.
 PN
 XX 01-FEB-2001.
 PD
 XX 14-JUL-2000; 2000WO-US019220.
 PF

CC determining region (HLA-DR) molecules and stimulate proliferation of
 CC helper T cells. The peptides can be administered to an HLA-DR positive
 CC subject in order to stimulate the helper T cells. An MHC Class II HLA-DR-
 CC NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in
 CC free form is useful for this stimulation. The nucleic acid is useful for
 CC screening for a cancerous condition, which involves contacting a subject
 CC sample to a cell line transfected with the immunoreactive cell (helper T
 CC cell), where interaction is indicative of cancer. In addition, a sample
 CC from a patient (for example, a body fluid or tissue) can be monitored for
 CC the amount of the complex present in the bloodstream. This is useful for
 CC determining regression, progression or onset of a cancerous condition.
 CC The method involves contacting the sample with a radioactive labelled or
 CC enzyme labelled monoclonal antibody which specifically binds with the
 CC complex
 CC
 XX Sequence 18 AA;
 SQ

Query Match 100.0%; Score 47; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.0084;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 Db 1 TVSGNLTIR 10
 |||||

RESULT 13
 AAU01540
 ID AAU01540 standard; peptide; 18 AA.
 XX
 AC AAU01540;
 DT 18-JUL-2001 (first entry)
 XX
 DE HLA-DR53 recognising NY-ESO-1 peptide #2.
 XX
 KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
 KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
 KW human leukocyte antigen-determining region; disease progression;
 KW disease regression; disease onset; body tissue; body fluid; enzyme label;
 KW radioactive label; monoclonal antibody.
 XX
 OS Homo sapiens.
 XX WO200123560-A2.
 PN
 PD 05-APR-2001.
 XX
 PF 26-SEP-2000; 2000WO-US026411.
 XX
 PR 29-SEP-1999; 99US-00408036.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Tureci O, Sahin U, Pfreundschuh M;
 XX WPI; 2001-266156/27.
 DR
 XX
 PT Polypeptides binding to major histocompatibility complex class II human
 PT leukocyte antigen-determining region molecule having amino acid sequence
 PT found in tumor rejection antigen precursor used for stimulating
 PT proliferation of helper T cells.
 PS
 XX Example 13; Page 19; 62pp; English.
 XX
 CC The sequence represents a human NY-ESO-1 tumour rejection antigen
 CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
 CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility
 CC complex (MHC) Class II molecules such as human leukocyte antigen-
 CC determining region (HLA-DR) molecules and stimulate proliferation of
 CC helper T cells. The peptides can be administered to an HLA-DR positive
 CC subject in order to stimulate the helper T cells. An MHC Class II HLA-DR-
 CC NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in

CC free form is useful for this stimulation. The nucleic acid is useful for
 CC screening for a cancerous condition, which involves contacting a subject
 CC sample to a cell line transfected with the immunoreactive cell (helper T
 CC cell), where interaction is indicative of cancer. In addition, a sample
 CC from a patient (for example, a body fluid or tissue) can be monitored for
 CC the amount of the complex present in the bloodstream. This is useful for
 CC determining regression, progression or onset of a cancerous condition.
 CC The method involves contacting the sample with a radioactive labelled or
 CC enzyme labelled monoclonal antibody which specifically binds with the
 CC complex
 CC
 XX Sequence 18 AA;
 SQ

Query Match 100.0%; Score 47; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.0084;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 Db 7 TVSGNLTIR 16
 |||||

RESULT 14
 AAE07769
 ID AAE07769 standard; peptide; 18 AA.
 XX
 AC AAE07769;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human NY ESO-1 HLA DR restricted T cell cancer peptide #1.
 XX
 KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
 KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 KW NY ESO-1 protein; CD4+ T lymphocyte; human leukocyte antigen; HLA;
 KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
 KW immunotherapy.
 XX
 OS Homo sapiens.
 XX WO200155393-A2.
 PN
 PD 02-AUG-2001.
 XX
 PF 26-JAN-2001; 2001WO-US002765.
 XX
 PR 28-JAN-2000; 2000US-0179004P.
 PR 29-SEP-2000; 2000US-0237107P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Wang R, Rosenberg SA, Zeng G;
 XX WPI; 2001-496851/54.
 DR
 XX
 PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis.
 PS
 XX Claim 84; Page 84; 134pp; English.
 XX
 CC The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also

CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any given
CC target antigen and/or hapten and to induce tumour-specific humoral-
CC mediated immunity against cancer. The present sequence is human NY ESO-1
CC HLA DR restricted T cell cancer peptide
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 7 TVSGNLTIR 16

RESULT 15
ADW50855
ID ADW50855 standard; peptide; 18 AA.
XX
AC ADW50855;
XX
DT 24-MAR-2005 (first entry)
XX
DE NY-ESO-1 peptide 121-138.
XX
KW cytostatic; immune stimulation; cancer; cytostatic; neoplasm; NY-ESO-1.
XX
OS Unidentified.
XX
PN WO2005000870-A2.
XX
PD 06-JAN-2005.
XX
PF 27-MAY-2004; 2004WO-US016849.
XX
PR 30-MAY-2003; 2003US-0474893P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PI Gnjatic S, Atanackovic D, Old LJ;
XX
DR WPI; 2005-066554/07.
XX

PT Novel NY-ESO-1 peptide that binds to human leukocyte antigen class II
PT molecules, useful for treating cancer.

PS Example 7; Page 12; 24pp; English.

XX The invention describes an isolated NY-ESO-1 peptide (I), consisting of
CC amino acids 80-109, 87-98, 108-119, 121-132 or 143-154 of a sequence of
CC 180 (S1) amino acids fully defined in the specification. Also described
CC are: a composition (II) useful in stimulating a CD4 + T cell response,
CC comprising (I) and an adjuvant; a composition (III) useful in stimulating
CC a T cell response in a subject, comprising (I) and at least one
CC additional peptide; an isolated nucleic acid molecule (IV) consisting of
CC a nucleotide sequence which encodes a peptide, where the amino acid
CC sequence is chosen from 80-109, 87-98, 108-119, 121-132 or 143-154 of 180
CC of (S1); an expression vector (V) comprising (IV) operably linked to a
CC promoter; a recombinant cell (VI) comprising (IV); a recombinant cell
CC (VII) comprising (V); and an isolated CD4 + T cell (VIII) which
CC recognizes a complex of (I) and a major histocompatibility complex (MHC)
CC Class II molecule. (I) is useful for treating cancer. This is the amino
CC acid sequence of a NY-ESO-1 peptide.
XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 47; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 7 TVSGNLTIR 16

Search completed: March 13, 2006, 19:03:56
Job time : 77.2941 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:04:24 ; Search time 11.8824 Seconds
(without alignments)
80.975 Million cell updates/sec

Title: US-09-529-206E-15
Perfect score: 47
Sequence: 1 TVSGNLTITR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	76.6	245	2 T13099	major tail protein
2	36	76.6	323	2 AD2753	lipoic Acid Synthetase
3	36	76.6	323	2 B97534	lipoic acid synthetase
4	35	74.5	335	2 A89837	hypothetical protein
5	34	72.3	177	1 R5BS0F	ribosomal protein
6	34	72.3	244	2 T41234	translation initiation
7	34	72.3	311	2 AB3218	2-hydroxyacid dehydrogenase
8	34	72.3	314	2 G86835	hypothetical protein
9	34	72.3	1266	2 A85989	hypothetical protein
10	34	72.3	1266	2 F91143	hypothetical protein
11	33	70.2	144	1 TPBPPI	tail fiber protein
12	33	70.2	144	2 S18683	gene R protein - E
13	33	70.2	411	2 G95241	MATE efflux family
14	33	70.2	426	2 B98106	hypothetical protein
15	33	70.2	428	2 F85253	hypothetical protein
16	33	70.2	436	2 B81033	N-acetylglutamate
17	33	70.2	436	2 A81977	probable amino-acyl transferase
18	33	70.2	449	2 S02011	serotonin receptor
19	33	70.2	471	2 A43956	serotonin receptor
20	33	70.2	471	2 S11280	serotonin receptor
21	33	70.2	471	2 S40689	5-hydroxytryptamin
22	33	70.2	471	2 A34863	serotonin receptor
23	33	70.2	876	2 E96674	hypothetical protein
24	33	70.2	918	2 T02759	hypothetical protein
25	33	70.2	1986	2 F71405	probable TMV resist
26	32	68.1	102	2 C86898	hypothetical protein
27	32	68.1	121	2 B81972	probable integral
28	32	68.1	135	2 D81029	conserved hypothetical
29	32	68.1	187	2 I37105	5-Htr2c receptor

30 32 68.1 234 2 H75390 hypothetical prote
31 32 68.1 245 2 S57550 hypothetical prote
32 32 68.1 289 2 C87158 probable oxidoredu
33 32 68.1 316 2 S25234 lysozyme (EC 3.2.1.1
34 32 68.1 344 2 A69325 hypothetical prote
35 32 68.1 347 2 G95146 conserved domain p
36 32 68.1 347 2 E98014 conserved hypothet
37 32 68.1 376 2 C97059 uncharacterized pr
38 32 68.1 418 2 E70401 S-adenosylhomocyst
39 32 68.1 451 2 S65162 hypothetical prote
40 32 68.1 455 1 HMXRS3 sigma 1 protein pr
41 32 68.1 458 2 JS0616 serotonin receptor
42 32 68.1 459 2 A43951 serotonin receptor
43 32 68.1 460 2 A32605 serotonin receptor
44 32 68.1 479 2 S23562 serotonin receptor
45 32 68.1 491 2 T30590 alkylhalidase homo

ALIGNMENTS

RESULT 1

T13099
major tail protein V - phage N15
N;Alternate names: protein gp13
C;Species: phage N15
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13099
R;Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, M.E.; Ravin, N.V.; Smirnov, I.K.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z17603
A;Accession: T13099
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-245 <HEN>
A;Cross-references: UNIPROT:O64327; UNIPARC:UPI000009BA91; EMBL:AF064539; NID:g3192683;
C;Genetics:
A;Note: Gene 13
C;Superfamily: phage lambda major tail protein V

Query Match 76.6%; Score 36; DB 2; Length 245;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TVSGNLTIT 9
Db 209 TVSGNLTIV 217

RESULT 2

AD2753
lipoic Acid Synthetase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 31-Dec-2004
C;Accession: AD2753
R;Wood, D.W.; Stuhel, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, Y.; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.E.
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD2753
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-323 <KUR>
A;Cross-references: UNIPROT:Q8UEG1; UNIPARC:UPI000012E6BE; GB:AE008688; PIDN:AAL42442.1
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: lipA
A;Map position: circular chromosome
C;Superfamily: lipoyl synthase

2-hydroxyacid dehydrogenase Atu5474 [imported] - Agrobacterium tumefaciens (strain C58,
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 05-Oct-2004
 C;Accession: AB3218
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: AB3218
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-311 <KUR>
 A;Cross-references: UNIPROT:Q8UUK3; UNIPARC:UPI0000167CD3; GB:AE008687; PIDN:AAL46160.1;
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: Atu5474
 A;Genome: plasmid
 C;Superfamily: 2-hydroxyacid dehydrogenase

Query Match 72.3%; Score 34; DB 2; Length 311;
 Best Local Similarity 77.8%; Pred. No. 44;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSGNLTIR 10
 |:|||||
 Db 288 VAGNLTIR 296

RESULT 8
 G86835
 hypothetical protein yreB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
 C;Species: Lactococcus lactis subsp. lactis
 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
 C;Accession: G86835
 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrli
 Genome Res. 11, 731-753, 2001
 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
 A;Reference number: A86625; MUID:21235186; PMID:11337471
 A;Accession: G86835
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-314 <STO>
 A;Cross-references: UNIPROT:Q9CEZ4; UNIPARC:UPI00000D449D; GB:AE005176; PID:g12724702; F
 A;Experimental source: strain IL1403
 C;Genetics:
 A;Gene: yreB

Query Match 72.3%; Score 34; DB 2; Length 314;
 Best Local Similarity 75.0%; Pred. No. 44;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSGNLTIR 9
 |:|||||
 Db 93 ISGNLTIR 100

RESULT 9
 A85989
 hypothetical protein Z4604 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
 C;Species: Escherichia coli
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C;Accession: A85989
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: A85989
 A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1266 <STO>

A;Cross-references: UNIPROT:Q8X9D5; UNIPARC:UPI00000D082E; GB:AE005174; NID:g12517869;
 A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: Z4604

C;Superfamily: Escherichia coli hypothetical protein yhdp

Query Match 72.3%; Score 34; DB 2; Length 1266;

Best Local Similarity 66.7%; Pred. No. 1.9e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9

|:|||||

Db 1017 TISGNLTIR 1025

RESULT 10

F91143

hypothetical protein ECs4118 [imported] - Escherichia coli (strain O157:H7, substrain R
 C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C;Accession: F91143

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
 gawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
 A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: F91143

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1266 <HAY>

A;Cross-references: UNIPROT:Q8X9D5; UNIPARC:UPI00000D082E; GB:BA000007; PIDN:BA037541.1
 A;Experimental source: strain O157:H7, substrain RMD 050952

C;Genetics:

A;Gene: ECs4118

C;Superfamily: Escherichia coli hypothetical protein yhdp

Query Match 72.3%; Score 34; DB 2; Length 1266;

Best Local Similarity 66.7%; Pred. No. 1.9e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9

|:|||||

Db 1017 TISGNLTIR 1025

RESULT 11

TPBPPI

tail fiber protein R - phage P1

C;Species: phage P1

C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004

C;Accession: JS0460

R;Guidolin, A.; Zingg, J.M.; Arber, W.

Gene 76, 239-243, 1989

A;Title: Organization of the bacteriophage P1 tail-fibre operon.

A;Reference number: PS0109; MUID:89326122; PMID:2526777

A;Accession: JS0460

A;Molecule type: DNA

A;Residues: 1-144 <GUI>

A;Cross-references: UNIPROT:P22946; UNIPARC:UPI0000138778; GB:M25470; NID:g341349; PIDN:
 C;Genetics:

A;Gene: R

C;Superfamily: phage P1 tail fiber protein R

C;Keywords: tail fiber

Query Match 70.2%; Score 33; DB 1; Length 144;

Best Local Similarity 60.0%; Pred. No. 31;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10

|:|||||

Db 79 TVSGGIIIVR 88

RESULT 12

S18683
 gene R protein - Escherichia coli plasmid p15B
 C:Species: Escherichia coli
 C:Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C:Accession: S18683
 R:Sandmeter, H.; Iida, S.; Huebner, P.; Hiestand-Nauer, R.; Arber, W.
 Nucleic Acids Res. 19, 5831-5838, 1991
 A:Title: Gene organization in the multiple DNA inversion region Min of plasmid p15B of E.
 A:Reference number: S18680; MUID:92051368; PMID:1945872
 A:Accession: S18683
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-144 <SAN>
 A:Cross-References: UNIPROT:Q47426; UNIPARC:UPI00000B4972; EMBL:X62121; NID:G42224; PIDN:
 C:Genetics:
 A:Gene: R
 A:Genome: plasmid
 C:Superfamily: phase P1 tail fiber protein R

Query Match 70.2%; Score 33; DB 2; Length 144;
 Best Local Similarity 60.0%; Pred. No. 31;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10

|||:|:|
 79 TVSGGIITVR 88

RESULT 13

G95241
 MATE efflux family protein [imported] - Streptococcus pneumoniae (strain TIGR4)
 C:Species: Streptococcus pneumoniae
 C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C:Accession: G95241
 R:Tetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
 neon, T.; Hickey, E.K.; Wolt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A:Reference number: A95000; MUID:21357209; PMID:11463916
 A:Accession: G95241
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-411 <KUR>
 A:Cross-References: UNIPROT:Q97NG5; UNIPARC:UPI0000051ADC; GB:AE005672; PIDN:AAK76128.1;
 A:Experimental source: strain TIGR4
 C:Genetics:
 A:Gene: SP2065

Query Match 70.2%; Score 33; DB 2; Length 411;
 Best Local Similarity 66.7%; Pred. No. 94;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9

|||:|:|
 30 SVAGNIITI 38

RESULT 14

B98106
 hypothetical protein MATE transporter [imported] - Streptococcus pneumoniae (strain R6)
 C:Species: Streptococcus pneumoniae
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: B98106
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;

A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A:Reference number: A97872; MUID:21429245; PMID:11544234

A:Accession: B98106
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-426 <KUR>
 A:Cross-References: UNIPROT:Q8DN77; UNIPARC:UPI00000E3724; GB:AE007317; PIDN:AAL00679.1
 C:Genetics:
 A:Gene: MATE transporter

Query Match 70.2%; Score 33; DB 2; Length 426;
 Best Local Similarity 66.7%; Pred. No. 98;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9

|||:|:|
 45 SVAGNIITI 53

RESULT 15

F85253
 hypothetical protein AT4g22170 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
 C:Accession: F85253
 R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
 Nature 402, 769-777, 1999
 A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A:Reference number: A85001; MUID:20083488; PMID:10617198
 A:Accession: F85253
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-428 <STO>
 A:Cross-References: UNIPROT:Q9SUG4; UNIPARC:UPI00000A1769; GB:NC_001268; NID:G7269062.1;
 C:Genetics:
 A:Gene: AT4g22170
 A:Map position: 4
 C:Superfamily: F-box containing protein

Query Match 70.2%; Score 33; DB 2; Length 428;
 Best Local Similarity 60.0%; Pred. No. 98;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10

|||:|:|
 316 TVTGNLRVQ 325

Search completed: March 13, 2006, 19:16:06
 Job time : 13.8824 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 18:53:23 ; Search time 72.5882 Seconds
(without alignments)
97.196 Million cell updates/sec

Title: US-09-529-206E-15
Perfect score: 47
Sequence: 1 TVSGNLTIR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	180	1	P78358 homo sapien
2	47	100.0	180	2	Q7LBY4 homo sapien
3	40	85.1	141	2	O670M2 SYNTH
4	39	83.0	142	2	Q9NY13 homo sapien
5	38	80.9	322	1	LIPA RHET
6	38	80.9	330	2	O5X5A2 LEGPA
7	38	80.9	617	2	Q4UGM9 THEAN
8	37	78.7	94	2	Q4UN39 RICFE
9	37	78.7	250	2	O8G743-BIFLO
10	37	78.7	330	2	Q5W877 LEGPL
11	37	78.7	334	2	Q5ZVH8 LEGPH
12	37	78.7	1217	2	O5AFQ7 CANAL
13	36	76.6	245	2	O64327 BPN15
14	36	76.6	318	2	O8EAQ4 SHEON
15	36	76.6	323	1	LIPA AGRT5
16	36	76.6	352	2	Q9YH74 LAMPL
17	36	76.6	450	2	Q9RY91 STRCO
18	36	76.6	1115	2	Q4NQF1 9DELT
19	35	74.5	143	1	ITBA2 HUMAN
20	35	74.5	143	2	O5HY39 HUMAN
21	35	74.5	144	2	Q8A5T8 BACTN
22	35	74.5	334	2	Q4L486 STRAHJ
23	35	74.5	335	2	O6GBG6 STRAAS
24	35	74.5	335	2	O6G3J6 STRAAR
25	35	74.5	335	2	O5HI04 STRAAC
26	35	74.5	335	2	Q7A1K9 STRAAR
27	35	74.5	335	2	Q932F0 STRAAM
28	35	74.5	335	2	Q99VV7 STRAAR
29	35	74.5	336	2	Q5HR76 STRABQ
30	35	74.5	336	2	Q8CQ35 STRABP
31	35	74.5	366	2	Q4SDU8_TETNG

RESULT 1

ID	CTG1B_HUMAN	STANDARD;	PRT;	180 AA.
AC	P78358;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-ESO-1).			
DE	ES0-1).			
GN	Name=CTAG1B; Synonym=CTAG, CTAG1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;			
RA	Chen Y.-T., Scanlan M.J., Sahin U., Tuerki O., Gure A.O., Tsang S.,			
RA	Williamson B., Stockert E., Pfundsckuh M., Old L.J.;			
RT	"A testicular antigen aberrantly expressed in human cancers detected			
RT	by autologous antibody screening."			
RL	Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Melanoma;			
RC	MEDLINE=98289662; PubMed=9626360;			
RA	Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,			
RA	de Plaen E., Boon T.;			
RT	"LAGE-1, a new gene with tumor specificity."			
RL	Int. J. Cancer 76:903-908(1998).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=98430682; PubMed=9759882;			
RA	Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,			
RA	Schwartzentruber D.J., Rosenberg S.A.;			
RT	"A breast and melanoma-shared tumor antigen: T cell responses to			
RT	antigenic peptides translated from different open reading frames."			
RL	J. Immunol. 161:3596-3606(1998).			
CC	-!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide			
CC	variety of cancers. Detected in uterine myometrium.			
CC	-!- SIMILARITY: Belongs to the CTAG family.			
CC	-----			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			
CC	-----			
DR	EMBL; U07459; AAB49693.1; -; mRNA.			
DR	EMBL; AJ003149; CAA05908.1; -; mRNA.			
DR	EMBL; AF038567; AAD05202.1; -; mRNA.			
DR	HGNC; HGNC:2491; CTAG1B.			
DR	MIM; 300156; -.			

O6LJS0 photobacter
O5WD6 legionella
O5X54 legionella
O5ZVD1 legionella
O5LNU4 silicibacte
O5LEA1 bacteroides
O9PT83 xenopus lae
O9PT82 xenopus lae
O6IRP9 xenopus lae
O6IRP9 xenopus lae
O6NX22 xenopus tro
O8T4D0 drosophila
O9VS00 drosophila
O9NEG0 drosophila
O93FV1 bacteroides

KW Antigen; Transmembrane.
 FT TRANSMEM 156 172 Potential.
 FT COMPIAS 5 82 Gly-rich.
 SQ SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 |||||
 Db 127 TVSGNLTIR 136

RESULT 4
 Q7LBY4 HUMAN
 ID Q7LBY4_HUMAN PRELIMINARY; PRT; 180 AA.
 AC Q7LBY4
 DT 10-MAY-2005 (TRENBLrel. 30, Created)
 DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
 DE Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis antigen 1-A).
 DE antigen 1-A.
 GN Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21303268;
 RA Galgoczy P., Rosenthal A., Platzer M.;
 RT "Human-mouse comparative sequence analysis of the NEMO gene reveals an alternative promoter within the neighboring G6PD gene.";
 RL Gene 271:93-98(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21566154; PubMed=11709543; DOI=10.1093/hmg/10.22.2557;
 RA Aradhyia S., Bardaro T., Galgoczy P., Yamagata T., Esposito T., Patlan H., Ciccocioppa A., Kenwick S., Platzer M., D'Urso M., Nelson D.L.;
 RT "Multiple pathogenic and benign genomic rearrangements occur at a 35 kb duplication involving the NEMO and LAGE2 genes.";
 RL Hum. Mol. Genet. 10:2557-2567(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Platzer M.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Platzer M.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA Galgoczy P., Platzer M.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99454989; PubMed=10523621;
 RA De Smet C., Larquin C., Lethe B., Martelange V., Boon T.;
 RT "DNA methylation is the primary silencing mechanism for a set of germ line- and tumor-specific genes with a CpG-rich promoter.";
 RL Mol. Cell. Biol. 19:7327-7335(1999).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RA Lethe B.G.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF277315; AAL27014.1; -; Genomic DNA.
 DR EMBL; AJ275977; CAB76943.1; -; Genomic DNA.
 DR EMBL; AF277315; AAL27013.1; -; Genomic DNA.
 SQ SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.55;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 |||||
 Db 127 TVSGNLTIR 136

RESULT 3
 Q67QW2 SYMTH
 ID Q67QW2_SYMTH PRELIMINARY; PRT; 141 AA.
 AC Q67QW2
 DT 25-OCT-2004 (TRENBLrel. 28, Created)
 DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
 DE Hsp20 family heat shock protein.
 GN OrderedLocusNames=STH946;
 OS Symbiobacterium thermophilum.
 OC Bacteria; Actinobacteria; Symbiobacterium.
 OX NCBI_TaxID=2734;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN-T / IAM 14863;
 RX PubMed=15383646; DOI=10.1093/nar/gkh830;
 RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T., Morimura K., Ikeda H., Hattori M., Beppu T.;
 RT "Genome sequence of Symbiobacterium thermophilum, an uncultivable bacterium that depends on microbial commensalism.";
 RL Nucleic Acids Res. 32:4937-4944(2004).
 CC -!- SIMILARITY: Belongs to the small heat shock protein (HSP20) family.
 CC EMBL; AP006840; BAD39931.1; -; Genomic DNA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR002068; Hsp20.
 DR Pfam; PF00011; HSP20; 1.
 DR PROSITE; PS01031; HSP20; 1.
 KW Complete proteome; Heat shock.
 SQ SEQUENCE 141 AA; 15725 MW; C7BA8A8CFC50FD36 CRC64;

Query Match 85.1%; Score 40; DB 2; Length 141;
 Best Local Similarity 80.0%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 |||||
 Db 67 TVDGNLTIR 76

RESULT 4
 Q9NY13 HUMAN
 ID Q9NY13_HUMAN PRELIMINARY; PRT; 142 AA.
 AC Q9NY13
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Hypothetical protein LAGE-2 (Fragment).
 GN Name=LAGE-2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Lethe B.G.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ275978; CAB76945.1; -; mRNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 142 AA; 13895 MW; 27BBE922AC4ACC7B CRC64;

Query Match 83.0%; Score 39; DB 2; Length 142;
Best Local Similarity 88.9%; Pred. No. 17;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9
|||
DB 101 TVSGNLTIR 109

RESULT 5
LIPA_RHET STANDARD; PRT; 322 AA.
ID LIPA_RHET
AC O05941;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Lipoyl synthase (EC 2.8.1.-) (Lipoic acid synthase) (Lipoate synthase)
DE (lipoyl-acyl-carrier protein synthase) (Sulfur insertion protein lipA)
DE (lip-syn).
GN Name=lipa;
OS Rhizobium etli.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=29449;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=CE3;
RX MEDLINE=97286510; PubMed=9141657; DOI=10.1016/S0378-1097(97)00069-4;
RA Tate R., Riccio A., Iaccarino M., Patriarca E.J.;
RT "Cloning and transcriptional analysis of the lipA (lipoic acid
synthetase) gene from Rhizobium etli.";
RL FEMS Microbiol. Lett. 149:165-172(1997).
CC -!- FUNCTION: Catalyzes the radical-mediated insertion of two sulfur
atoms into an octanoyl group bound to acyl carrier protein (ACP)
to produce a lipoyl group (By similarity).
CC -!- CATALYTIC ACTIVITY: octanoyl-[acyl-carrier protein] + 2 sulfurs =
lipoyl-[acyl-carrier protein].
CC -!- COFACTOR: Binds 1 4Fe-4S cluster coordinated with 3 cysteines and
an exchangeable S-adenosyl-L-methionine (By similarity).
CC -!- COFACTOR: Binds 1 3Fe-4S cluster (Potential).
CC -!- PATHWAY: Lipoate biosynthesis; sulfur-insertion step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the biotin and lipoic acid synthetases
family. LipA subfamily.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

EMBL; Y11708; CAAT2400.1; -; Genomic_DNA.

DR HAMAP; MF_00206; -; 1.
DR InterPro; IPR006638; Elp3/MiAB/NiFe.
DR InterPro; IPR003698; Lipoate synth.
DR InterPro; IPR007197; Radical_SAM.
DR PANTHER; PTHR10949; Lipoate synth; 1.
DR Pfam; PF04055; Radical_SAM; 1.
DR PIRSF; PIRSF005963; Lipoyl synth; 1.
DR SMART; SM00729; Elp3; 1.
DR TIGRFAMs; TIGR00510; lipA; 1.
KW 3Fe-4S; 4Fe-4S; Iron; Iron-sulfur; Metal-binding; Transferase.
FT METAL 61 61 Iron-sulfur 1 (3Fe-4S) (Potential).
FT METAL 66 66 Iron-sulfur 1 (3Fe-4S) (Potential).
FT METAL 72 72 Iron-sulfur 1 (3Fe-4S) (Potential).
FT METAL 87 87 Iron-sulfur 2 (4Fe-4S-S-AdoMet) (By
similarity).
FT METAL 91 91 Iron-sulfur 2 (4Fe-4S-S-AdoMet) (By
similarity).
FT METAL 94 94 Iron-sulfur 2 (4Fe-4S-S-AdoMet) (By
similarity).
FT SEQUENCE 322 AA; 36298 MW; 45E7185215486847 CRC64;

Query Match 80.9%; Score 38; DB 1; Length 322;
Best Local Similarity 70.0%; Pred. No. 61;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
|||
DB 188 TVAGNLTIR 197

RESULT 6
Q5X5A2 LEGPA
ID Q5X5A2 LEGPA PRELIMINARY; PRT; 330 AA.
AC Q5X5A2;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Hypothetical protein.
DE OrderedLocNames=lppl418;
GN Legionella pneumophila (strain Paris).
OS Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297246;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15467720; DOI=10.1038/ng1447;
RA Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA Etienne J., Glaser P., Buchrieser C.;
RT "Evidence in the Legionella pneumophila genome for exploitation of
host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
DR EMBL; CR628336; CAH12569.1; -; Genomic_DNA.
DR LegioLst; lppl418; -.
DR GO; GO:0050660; F:AD binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008033; P:tRNA processing; IEA.
DR InterPro; IPR001369; Du_synth.
DR Pfam; PF01207; Duf; 1.
DR PROSITE; PS01136; UPR0034; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 330 AA; 37270 MW; 9BCB4B74CD8B383 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 330;
Best Local Similarity 77.8%; Pred. No. 63;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9
|||
DB 204 TINGNLTIR 212

RESULT 7
Q4UGM9 THEAN
ID Q4UGM9 THEAN PRELIMINARY; PRT; 617 AA.
AC Q4UGM9;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Theileria parva Tpr-related protein, putative.
GN ORFNames=TA21390;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC Theileria.
OX NCBI_TaxID=5874;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
RA Hall N., Barrall B.G.;
RT "The chromosome 1 sequence of Theileria annulata.";
RL Submitted (APR-2005) to the EMBL/GenBank/DDJ databases.
DR EMBL; CR940347; CAI73760.1; -; Genomic DNA.
SQ SEQUENCE 617 AA; 67272 MW; 2A3696230D209B70 CRC64;

```
Query Match      80.9%; Score 38; DB 2; Length 617;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
   |.|||||
Db 451 TISGNLTIR 460

RESULT 8
Q4UN39_RICFE
ID Q4UN39_RICFE PRELIMINARY; PRT; 94 AA.
AC Q4UN39;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=RF_0168;
OS Rickettsia felis (Rickettsia azadi).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia; spotted fever group.
OX NCBI_TaxID=42862;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=URRWKcal2;
RX PubMed=15984913; DOI=10.1371/journal.pbio.0030248;
RA Ogata H., Renseto P., Audic S., Robert C., Blanc G., Fournier P.-E.,
RA Parinello H., Claverie J.-M., Raoult D.;
RT "The genome sequence of Rickettsia felis identifies the first putative
RT conjugative plasmid in an obligate intracellular parasite.";
RL PLOS Biol. 3:E248-E248(2005).
DR EMBL; CP000053; AAY61019.1; -; Genomic_DNA.
DR InterPro; IPR007460; DUF497.
DR Pfam; PF04365; DUF497; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 94 AA; 11378 MW; D62F3C1DE3CF686E CRC64;

Query Match      78.7%; Score 37; DB 2; Length 94;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSGNLTIR 10
   |.|||||
Db 56 VDGNLTIR 64

RESULT 9
Q8G743_BIFLO
ID Q8G743_BIFLO PRELIMINARY; PRT; 250 AA.
AC Q8G743;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Possible cobyric acid synthase CobQ.
GN OrderedLocusNames=BL0429;
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL; AE014295; AAN24266.1; -; Genomic DNA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0009236; P:cobalamin biosynthesis; IEA.
```

```
DR InterPro; IPR011698; GATase_3.
DR Pfam; PF07685; GATase_3; 1.
SQ SEQUENCE 250 AA; 27653 MW; 7577954A609689CF CRC64;

Query Match      78.7%; Score 37; DB 2; Length 250;
Best Local Similarity 87.5%; Pred. No. 75;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGNLTIR 10
   |.|||||
Db 21 SGNLTIR 28

RESULT 10
Q5WM87_LEGPH
ID Q5WM87_LEGPH PRELIMINARY; PRT; 330 AA.
AC Q5WM87;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=lp11566;
OS Legionella pneumophila (strain Lens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297245;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15467720; DOI=10.1038/ng1447;
RA Cazalet C., Ruenik C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Buchrieser C.;
RA Etienne J., Glaser P., Buchrieser C.;
RT "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
DR EMBL; CR628337; CAH15806.1; -; Genomic_DNA.
DR LegiOList; lp11566; -.
DR GO; GO:0050660; F:FAD binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008033; P:tRNA processing; IEA.
DR InterPro; IPR001269; Du_synth.
DR Pfam; PF01207; Dus; 1.
DR PROSITE; PS01136; UPF0034; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 330 AA; 37311 MW; BEF836DAF152E15E CRC64;

Query Match      78.7%; Score 37; DB 2; Length 330;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9
   |.|||||
Db 204 TINGNLTIV 212

RESULT 11
Q5ZVH8_LEGPH
ID Q5ZVH8_LEGPH PRELIMINARY; PRT; 334 AA.
AC Q5ZVH8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Zinc binding TIM barrel protein, YjBN family.
GN OrderedLocusNames=lp1462;
OS Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /
OS ATCC 33152).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=272624;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15448271; DOI=10.1126/science.1099776;
```

RA Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,
RA Asamani G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.J.,
RA Steahenko V., Park S.H., Zhao B., Tepitskaya E., Edwards J.R.,
RA Pampou S., Georgiou A., Chou I.-C., Iannuccilli W., Ulz M.E.,
RA Km D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,
RA Segal G., Qu X., Rzhetsky A., Zhang P., Cavanis E., De Jong P.J.,
RA Ju J., Kalachikov S., Shuman H.A., Russo J.J.;
RT "The genomic sequence of the accidental pathogen Legionella
RT pneumophila";
RL Science 305:1966-1968(2004).
DR EMBL; AE017354; AAU27544.1; -; Genomic_DNA.
DR GO; GO:0050660; F:PAD binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008033; P:RNA processing; IEA.
DR InterPro; IPR001269; Du_synth.
DR Pfam; PF01207; Dus; 1.
DR PROSITE; PS01136; UPF0034; 1.
DR Complete proteome.
SQ SEQUENCE 334 AA; 37796 MW; 4B216C11814E0ADD CRC64;

Query Match 78.7%; Score 37; DB 2; Length 334;
Best Local Similarity 66.7%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
Matches 6; Conservative 3; Mismatches 0;

Qy 1 TVSGNLTIT 9
Db 208 TINGNLTIV 216
:::|||||:

RESULT 12
Q5AFQ7 CANAL
ID Q5AFQ7 CANAL PRELIMINARY; PRT; 1217 AA.
AC Q5AFQ7
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Ca019.7011;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Trung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotation of the Genome of Candida albicans";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear; nucleolar (By similarity).
DR EMBL; AACQ01000024; EAL01458.1; -; Genomic_DNA.
DR InterPro; IPR011989; ARM-like.
DR InterPro; IPR012978; DUF_NUC173.
DR InterPro; IPR000357; HEAT.
DR Pfam; PF02985; HEAT; 2.
DR Pfam; PF08161; NUC173; 1.
DR Complete proteome.
KW Hypothetical protein; Transmembrane.
SQ SEQUENCE 1217 AA; 135897 MW; 1F2788D13CAD6DEC CRC64;

Query Match 78.7%; Score 37; DB 2; Length 1217;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIT 9
Db 636 TIAGNLTIV 644
:::|||||:

RESULT 13
O64327 BPN15
ID O64327 BPN15 PRELIMINARY; PRT; 245 AA.
AC O64327;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gp13.
GN Name-gene 13;
OS Bacteriophage N15.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC N15-like viruses.
OX NCBI_TaxID=40631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hendrix R.W., Ravin V.K., Casjens S.R., Ford M.E., Ravin N.V.,
RA Smirnov I.K.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF064539; AAC19050.1; -; Genomic_DNA.
DR PIR; T13099; T13099.
DR InterPro; IPR003343; Big_2.
DR Pfam; PF02368; Big_2; 1.
DR SMART; SM00635; Bid_2; 1.
SQ SEQUENCE 245 AA; 25571 MW; 2CC941997C103FD3 CRC64;

Query Match 76.6%; Score 36; DB 2; Length 245;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TVSGNLTIT 9
Db 209 TVSGNLTIV 217
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RESULT 14
Q8EAQ4 SHEON
ID Q8EAQ4 SHEON PRELIMINARY; PRT; 318 AA.
AC Q8EAQ4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SO3842.
GN OrderedLocusNames=SO3842;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Neilson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis";
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AE015617; AAN56819.1; -; Genomic_DNA.
DR TIGR; SO3842; -.
KW Complete proteome.
SQ SEQUENCE 318 AA; 34113 MW; 0A0B7165033B6FCF CRC64;

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Query Match          76.6%; Score 36; DB 2; Length 318;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY      1 TVSGNLTIR 8
Db      153 TVSGNLTIR 160

RESULT 15
LIPA AGRT5
ID      LIPA AGRT5      STANDARD;      PRT;      323 AA.
AC      Q8URGL;
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      13-FEB-2003 (Rel. 41, Last sequence update)
DT      13-SEP-2005 (Rel. 48, Last annotation update)
DE      Lipoyl synthase (SC 2.8.1.-) (Lipoic acid synthase) (lipoate synthase)
DE      (Lipoyl-acyl-carrier protein synthase) (Sulfur insertion protein lipo)
DE      (lip-syn).
GN      Name=LIPA; OrderedLocusNames=Atul436, AGR_C_2646;
OS      Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC      Rhizobiaceae; Agrobacterium.
OX      NCBI_TaxID=176299;
RN      [1]_TaxID=176299;
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX      MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA      Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA      Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA      Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA      Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA      Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Gordon D.,
RA      Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA      Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA      Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA      Chumley P., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA      Nester E.W.;
RT      "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT      C58."
RL      Science 294:2317-2323 (2001).
RN      [2]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX      MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA      Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,
RA      Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA      Houmief K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA      Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA      Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA      Cielo C., Slater S.;
RT      "Genome sequence of the plant pathogen and biotechnology agent
RT      Agrobacterium tumefaciens C58."
RL      Science 294:2323-2328 (2001).
CC      -!- FUNCTION: Catalyzes the radical-mediated insertion of two sulfur
CC      atoms into an octanoyl group bound to acyl carrier protein (ACP)
CC      to produce a lipoyl group (By similarity).
CC      -!- CATALYTIC ACTIVITY: octanoyl-[acyl-carrier protein] + 2 sulfurs =
CC      lipoyl-[acyl-carrier protein].
CC      -!- COFACTOR: Binds 1 4Fe-4S cluster coordinated with 3 cysteines and
CC      an exchangeable S-adenosyl-L-methionine (By similarity).
CC      -!- COFACTOR: Binds 1 3Fe-4S cluster (Potential).
CC      -!- PATHWAY: lipoate biosynthesis; sulfur-insertion step.
CC      -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC      -!- SIMILARITY: Belongs to the biotin and lipoic acid synthetases
CC      family. LipoA subfamily.
-----
This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
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EMBL; AE009104; AAL42442.1; -; Genomic DNA.
EMBL; AE008069; AAK87227.1; -; Genomic DNA.

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DR      PIR; AD2753; AD2753.
DR      PIR; B97534; B97534.
DR      HAMAP; MF_00206; -; 1.
DR      InterPro; IPR006638; Elp3/MiaB/NifB.
DR      InterPro; IPR003698; Lipoate synth.
DR      InterPro; IPR007197; Radical_SAM.
DR      PANTHER; PTHR10949; Lipoate_synth; 1.
DR      Pfam; PF04055; Radical_SAM; 1.
DR      PIRSF; PIRSF005963; Lipoyl_synth; 1.
DR      SMART; SM00729; Elp3; 1.
DR      TIGRFAMs; TIGR00510; lipoA; 1.
KW      3Fe-4S; 4Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding;
KW      Transferase.
FT      METAL 61 61 Iron-sulfur 1 (3Fe-4S) (Potential).
FT      METAL 66 66 Iron-sulfur 1 (3Fe-4S) (Potential).
FT      METAL 72 72 Iron-sulfur 1 (3Fe-4S) (Potential).
FT      METAL 87 87 Iron-sulfur 2 (4Fe-4S-S-AdoMet) (By
FT      similarity).
FT      METAL 91 91 Iron-sulfur 2 (4Fe-4S-S-AdoMet) (By
FT      similarity).
FT      METAL 94 94 Iron-sulfur 2 (4Fe-4S-S-AdoMet) (By
FT      similarity).
SQ      SEQUENCE 323 AA; 36341 MW; 74B294773BC784D2 CRC64;

Query Match          76.6%; Score 36; DB 1; Length 323;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CY      1 TVSGNLTIR 10
Db      189 TVPGNLTIVR 198

Search completed: March 13, 2006, 19:14:21
Job time : 75.5882 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:14:49 ; Search time 18.5882 Seconds
(without alignments)
44.477 Million cell updates/sec

Title: US-09-529-206E-15

Perfect score: 47

Sequence: 1 TVSGNLTIR 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	18	2	US-09-359-503-9
2	47	100.0	18	2	US-09-359-503-13
3	47	100.0	18	2	US-09-165-546D-9
4	47	100.0	18	2	US-09-165-546D-13
5	47	100.0	18	2	US-09-408-036B-8
6	47	100.0	18	2	US-09-408-036B-12
7	47	100.0	180	1	US-08-937-263B-8
8	47	100.0	180	2	US-09-751-495-9
9	47	100.0	180	2	US-09-751-798-8
10	47	100.0	180	2	US-09-392-714-25
11	47	100.0	180	2	US-09-165-546D-15
12	47	100.0	180	2	US-09-341-829A-9
13	47	100.0	180	2	US-09-849-602-30
14	42	89.4	9	2	US-09-344-040C-125
15	42	89.4	9	2	US-09-833-039A-125
16	38	80.9	9	2	US-09-344-040C-120
17	38	80.9	9	2	US-09-833-039A-120
18	38	80.9	180	1	US-08-791-495-7
19	38	80.9	180	2	US-09-341-829A-7
20	37	78.7	574	2	US-09-248-796A-16162
21	35	74.5	342	2	US-09-134-001C-5428
22	34	72.3	149	2	US-09-540-236-2614
23	34	72.3	177	2	US-09-732-210-1076
24	34	72.3	185	2	US-09-270-767-58027
25	34	72.3	379	2	US-09-270-767-42707
26	34	72.3	585	2	US-10-104-047-2739
27	33	70.2	97	1	US-08-118-270-329

28 33 70.2 97 4 PCT-US93-08528-329 Sequence 329, Appl
29 33 70.2 109 2 US-09-341-461-35 Sequence 35, Appl
30 33 70.2 362 2 US-09-134-001C-5209 Sequence 5209, Appl
31 33 70.2 379 1 US-08-118-270-32 Sequence 32, Appl
32 33 70.2 379 4 PCT-US93-08528-32 Sequence 32, Appl
33 33 70.2 426 2 US-09-583-110-4783 Sequence 4783, Appl
34 33 70.2 426 2 US-09-769-787-34 Sequence 34, Appl
35 33 70.2 434 2 US-09-107-433-3247 Sequence 3247, Appl
36 33 70.2 470 2 US-09-292-071-25 Sequence 25, Appl
37 33 70.2 470 2 US-09-292-069A-25 Sequence 25, Appl
38 33 70.2 470 2 US-09-767-013-25 Sequence 25, Appl
39 33 70.2 470 2 US-09-292-072-25 Sequence 25, Appl
40 33 70.2 470 2 US-10-176-255-25 Sequence 25, Appl
41 33 70.2 471 1 US-07-817-920-8 Sequence 8, Appl
42 33 70.2 471 1 US-07-996-772A-11 Sequence 11, Appl
43 33 70.2 471 1 US-08-370-542-7 Sequence 7, Appl
44 33 70.2 471 1 US-08-117-006-8 Sequence 8, Appl
45 33 70.2 471 1 US-08-216-594-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1

US-09-359-503-9
; Sequence 9, Application US/09359503
; Patent No. 6251603

GENERAL INFORMATION:

; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;

; APPLICANT: Knuth, alexander

; TITLE OF INVENTION: Method for Determining Status of A

; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies

; TITLE OF INVENTION: a Patient Sample

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fulbright & Jaworski, L.L.P.

; CITY: New York City

; STATE: New York

; COUNTRY: USA

; ZIP: 10103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: WordPerfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09359,503

; FILING DATE: July 23, 1999

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/165,546

; FILING DATE: October 2, 1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/062,422

; FILING DATE: April 17, 1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/937,263

; FILING DATE: September 15, 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/752,182

; FILING DATE: 03-October-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, No. 6251603man D.

; REGISTRATION NUMBER: 30,946

; REFERENCE/DOCKET NUMBER: LUD 5466.1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 318-3000

; TELEFAX: (212) 752-5958

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

TOPOLOGY: linear
US-09-359-503-9

Query Match 100.0%; Score 47; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 7 TVSGNLTIR 16

RESULT 2

US-09-359-503-13
Sequence 13, Application US/09359503
Patent No. 6251603
GENERAL INFORMATION:
APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Knuth, Alexander
TITLE OF INVENTION: Method for Determining Status of A
TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
TITLE OF INVENTION: a Patient Sample
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,503
FILING DATE: July 23, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/165,546
FILING DATE: October 2, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6251603man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-09-359-503-13

Query Match 100.0%; Score 47; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 1 TVSGNLTIR 10

RESULT 3

US-09-165-546D-9
Sequence 9, Application US/09165546D
Patent No. 6723832
GENERAL INFORMATION:
APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CT
USSES THEREOF

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10158

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Word

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-Oct-1998
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998

APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6723832man D.
REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 318-3400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-165-546D-9

Query Match 100.0%; Score 47; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 7 TVSGNLTIR 16

RESULT 4

US-09-165-546D-13
Sequence 13, Application US/09165546D
Patent No. 6723832
GENERAL INFORMATION:

APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
Gure, Ali, Old, Lloyd, Ritter, Gerd
TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CT
USSES THEREOF

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue


```

Db      7 TVSGNLTIR 16

RESULT 6
US-09-408-036B-12
; Sequence 12, Application US/09408036B
; Patent No. 6800730
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfeundschnuh, Michael
; TITLE OF INVENTION: Isolated peptides which bind to MHC Class II Molecules and Use
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/09/408,036B
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-408-036B-12

Query Match      100.0%; Score 47; DB 2; Length 18;
Best Local Similarity 100.0%; Pred No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TVSGNLTIR 10
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Db      1 TVSGNLTIR 10

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RESULT 7
US-08-791-495-9
: Sequence 9, Application US/08791495
: Patent No. 5811519
: GENERAL INFORMATION:
: APPLICANT: Leth , Bernard
: APPLICANT: Lucas, Sophie
: APPLICANT: De Smet, Charles
: APPLICANT: Godelaine, Daniele
: APPLICANT: Boon-Falleur, Thierry
: TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
: STREET: 600 Atlantic Avenue
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/791,495
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Van Amsterdam, John R.
: REGISTRATION NUMBER: 40,212
: REFERENCE/DOCKET NUMBER: L0461/7005
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-720-3500
: TELEFAX: 617-720-2441
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 180 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 47; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 1 TVSGNLTIR 10
Db 127 TVSGNLTIR 136

RESULT 8
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tsang; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751.798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6525177man D.
; REGISTRATION NUMBER: 30,945
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-09-751-798-8

Query Match 100.0%; Score 47; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 1 TVSGNLTIR 10
Db 127 TVSGNLTIR 136

RESULT 10
US-09-392-714-25
; Sequence 25, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tsang
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 180
; TYPE: PRT

US-08-937-263B-8

Query Match 100.0%; Score 47; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

QY 1 TVSGNLTIR 10
Db 127 TVSGNLTIR 136

RESULT 9
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
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; ORGANISM: Homo sapiens
US-09-392-714-25

Query Match      100.0%; Score 47; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TVSGNLTIR 10
Db      127 TVSGNLTIR 136

RESULT 11
US-09-165-546D-15
; Sequence 15, Application US/09165546D
; Patent No. 6723832
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
; USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546D
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6723832man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15

Query Match      100.0%; Score 47; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TVSGNLTIR 10
Db      127 TVSGNLTIR 136

RESULT 12
US-09-341-829A-9
; Sequence 9, Application US/09341829A
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; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Palleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-9

Query Match      100.0%; Score 47; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TVSGNLTIR 10
Db      127 TVSGNLTIR 136

RESULT 13
US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30

Query Match      100.0%; Score 47; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TVSGNLTIR 10
Db      127 TVSGNLTIR 136

RESULT 14
US-09-344-040C-125
; Sequence 125, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determini
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
; TITLE OF INVENTION: Gene, and Uses Thereof
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; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 125
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-125
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Query Match      89.4%; Score 42; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 TVSGNILTI 9
Db      1 TVSGNILTI 9
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RESULT 15
US-09-833-039A-125
; Sequence 125, Application US/09833039A
; Patent No. 6673350.
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 125
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-125
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Query Match      89.4%; Score 42; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 TVSGNILTI 9
Db      1 TVSGNILTI 9
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Search completed: March 13, 2006, 19:18:49
Job time : 18.5882 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:51:56 ; Search time 60.4706 Seconds
(without alignments)
69.096 Million cell updates/sec

Title: US-09-529-206E-15
Perfect score: 47
Sequence: 1 TVSGNLTIR 10

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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
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4: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	14	5	US-10-182-506A-17
2	47	100.0	15	5	US-10-182-506A-15
3	47	100.0	15	5	US-10-182-506A-16
4	47	100.0	18	4	US-10-751-088-9
5	47	100.0	18	4	US-10-751-088-13
6	47	100.0	18	4	US-10-851-884-8
7	47	100.0	18	4	US-10-851-884-12
8	47	100.0	18	5	US-10-182-506A-65
9	47	100.0	20	4	US-10-164-121A-35
10	47	100.0	20	4	US-10-164-078A-34
11	47	100.0	20	5	US-10-182-506A-38
12	47	100.0	20	5	US-10-941-150A-35
13	47	100.0	25	5	US-10-491-891-83
14	47	100.0	25	5	US-10-182-506A-7
15	47	100.0	27	5	US-10-182-506A-6
16	47	100.0	30	4	US-10-296-734-1414
17	47	100.0	54	4	US-10-447-161-1410
18	47	100.0	123	4	US-10-777-053-17
19	47	100.0	123	4	US-10-837-217-17
20	47	100.0	179	4	US-10-777-053-20
21	47	100.0	179	4	US-10-837-217-20
22	47	100.0	179	5	US-10-482-029-202
23	47	100.0	180	3	US-09-751-798-8
24	47	100.0	180	3	US-09-849-602-30
25	47	100.0	180	4	US-10-023-182-8
26	47	100.0	180	4	US-10-207-655-71
27	47	100.0	180	4	US-10-026-066-3

28	47	100.0	180	4	US-10-117-937-74	Sequence 74, Appl
29	47	100.0	180	4	US-10-295-027-386	Sequence 386, App
30	47	100.0	180	4	US-10-296-734-832	Sequence 832, App
31	47	100.0	180	4	US-10-188-832-139	Sequence 139, App
32	47	100.0	180	4	US-10-777-053-11	Sequence 11, Appl
33	47	100.0	180	4	US-10-751-088-15	Sequence 15, Appl
34	47	100.0	180	4	US-10-657-022-74	Sequence 74, Appl
35	47	100.0	180	4	US-10-837-217-11	Sequence 11, Appl
36	47	100.0	180	5	US-10-877-373-9	Sequence 9, Appli
37	47	100.0	180	5	US-10-723-860-1270	Sequence 1270, Ap
38	47	100.0	180	5	US-10-871-708-7	Sequence 7, Appli
39	47	100.0	180	5	US-10-895-523-3	Sequence 3, Appli
40	47	100.0	180	5	US-10-182-506A-3	Sequence 3, Appli
41	47	100.0	180	5	US-10-756-149-5024	Sequence 5024, Ap
42	47	100.0	180	6	US-11-067-064-74	Sequence 74, Appl
43	47	100.0	180	6	US-11-067-159-74	Sequence 74, Appl
44	47	100.0	397	3	US-09-821-883-27	Sequence 27, Appl
45	47	100.0	397	6	US-11-144-912-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-10-182-506A-17
; Sequence 17, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; TITLE OF INVENTION: ANTIGEN, NY ESO-1
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-17
Query Match 100.0%; Score 47; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TVSGNLTIR 10
DB 4 TVSGNLTIR 13
RESULT 2
US-10-182-506A-15
; Sequence 15, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; TITLE OF INVENTION: ANTIGEN, NY ESO-1
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A

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; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/027655
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
JS-10-182-506A-15

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Query Match      100.0%; Score 47; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.03,
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 TVSGNLTIR 10
Db 6 TVSGNLTIR 15

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RESULT 3
US-10-182-506A-16
; Sequence 16, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; TITLE OF INVENTION: ANTIGEN, NY ESO-1
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182.506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-16

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Query Match      100.0%; Score 47; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 10: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 TVSGNLTIR 10
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Db 5 TVSGNLTIR 14

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RESULT 4
US-10-751-088-9
; Sequence 9, Application US/10751088
; Publication NO. US20040158044A1
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CLASS II

```

1 USES THEREOF
 2
 3 NUMBER OF SEQUENCES: 15
 4 CORRESPONDENCE ADDRESS:
 5 ADDRESSEE: FULBRIGHT & JAWORSKI LLP
 6 STREET: 666 Fifth Avenue
 7 CITY: New York City
 8 STATE: New York
 9 COUNTRY: USA
 10 ZIP: 10158
 11
 12 COMPUTER READABLE FORM:
 13 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 14 COMPUTER: IBM
 15 OPERATING SYSTEM: PC-DOS
 16 SOFTWARE: Word
 17
 18 CURRENT APPLICATION DATA:
 19 APPLICATION NUMBER: US/10/751,088
 20 FILING DATE: 02-Jan-2004
 21 CLASSIFICATION: 530
 22
 23 PRIOR APPLICATION DATA:
 24 APPLICATION NUMBER: US/09/165,546D
 25 FILING DATE: 02-Oct-1998
 26 APPLICATION NUMBER: 09/062,422
 27 FILING DATE: April 17, 1998
 28 APPLICATION NUMBER: 08/937,263
 29 FILING DATE: September 15, 1997
 30 APPLICATION NUMBER: US 08/725,182
 31 FILING DATE: October 3, 1996
 32
 33 ATTORNEY/AGENT INFORMATION:
 34 NAME: Hanson, Norman D.
 35 REGISTRATION NUMBER: 30,946
 36 REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811-7)
 37
 38 TELECOMMUNICATION INFORMATION:
 39 TELEPHONE: (212) 318-3000
 40 TELEFAX: (212) 318-3400
 41
 42 INFORMATION FOR SEQ ID NO: 9:
 43 SEQUENCE CHARACTERISTICS:
 44 LENGTH: 18 amino acids
 45 TYPE: amino acid
 46 TOPOLOGY: linear
 47
 48 SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 49 PS-10-751-088-9

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Query Match      100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 TVSGNLTIR 10
Db 7 TVSGNLTIR 16

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RESULT 5
US-10-751-088-13
; Sequence 13, Application US/10751088
; Publication No. US20040158044A1
;
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
;           Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                     SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS
;                     USES THEREOF
;
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS

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SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/751,088
FILING DATE: 02-Jan-2004
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-Oct-1998
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 318-3400
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-751-088-13

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 1 TVSGNLTIR 10

RESULT 6

US-10-851-884-8
Sequence 8, Application US/10851884
Publication No. US20040214284A1
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfeundschnuh, Michael
TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses
FILE REFERENCE: LUD 5624
CURRENT APPLICATION NUMBER: US/10/851,884
PRIOR FILING DATE: 2004-05-21
PRIOR APPLICATION NUMBER: US/09/408,036
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 09/344,040
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/165,546
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 8
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-10-851-884-8

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 7 TVSGNLTIR 16

RESULT 7

US-10-851-884-12
Sequence 12, Application US/10851884
Publication No. US20040214284A1
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfeundschnuh, Michael
TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses
FILE REFERENCE: LUD 5624
CURRENT APPLICATION NUMBER: US/10/851,884
PRIOR FILING DATE: 2004-05-21
PRIOR APPLICATION NUMBER: US/09/408,036
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 09/344,040
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/165,546
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 12
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-10-851-884-12

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 1 TVSGNLTIR 10

RESULT 8

US-10-182-506A-65
Sequence 65, Application US/10182506A
Publication No. US20050136402A1
GENERAL INFORMATION:
APPLICANT: Wang, R-F
APPLICANT: Rosenberg, S A
APPLICANT: Zeng, G
TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
TITLE OF INVENTION: ANTIGEN, NY ESO-1
FILE REFERENCE: 217955
CURRENT APPLICATION NUMBER: US/10/182,506A
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: PCT/US01/02765
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/179,004
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/237,107
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
SEQ ID NO 65
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-182-506A-65

Query Match 100.0%; Score 47; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 7 TVSGNLTIR 16

RESULT 9

US-10-164-121A-35

; Sequence 35, Application US/10164121A
; Publication No. US20030228308A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Boon, Thierry
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Traversari, Catra
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-Cw6 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5771
; CURRENT APPLICATION NUMBER: US/10/164,121A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 35
; LENGTH: 20
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; US-10-164-121A-35

Query Match 100.0%; Score 47; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 9 TVSGNLTIR 18

RESULT 10

US-10-164-078A-34
; Sequence 34, Application US/10164078A
; Publication No. US20030228325A1
; GENERAL INFORMATION:
; APPLICANT: Bilsborough, Janine
; APPLICANT: Schultz, Erwin
; APPLICANT: Panichelli, Christophe
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B18 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5756
; CURRENT APPLICATION NUMBER: US/10/164,078A
; CURRENT FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 34
; LENGTH: 20
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
; US-10-164-078A-34

Query Match 100.0%; Score 47; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 9 TVSGNLTIR 18

RESULT 11

US-10-182-506A-38
; Sequence 38, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; TITLE OF INVENTION: ANTIGEN, NY ESO-1
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765

; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-182-506A-38

Query Match 100.0%; Score 47; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 2 TVSGNLTIR 11

RESULT 12

US-10-941-150A-35
; Sequence 35, Application US/10941150A
; Publication No. US20050226881A1
; GENERAL INFORMATION:
; APPLICANT: VAN DER BRUGGEN, Pierre
; APPLICANT: BOON-FALLEUR, Thierry
; APPLICANT: BRECKPOT, Karine
; APPLICANT: THIELEMAN, Kris
; TITLE OF INVENTION: ISOLATED PEPTIDE WHICH BINDS TO HLA-CW*07 AND USES THEREOF
; FILE REFERENCE: LUD-5853-US (10411307)
; CURRENT APPLICATION NUMBER: US/10/941,150A
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: US 60/504,874
; PRIOR FILING DATE: 2003-09-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from NY-ESO-1
; US-10-941-150A-35

Query Match 100.0%; Score 47; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 9 TVSGNLTIR 18

RESULT 13

US-10-491-891-83
; Sequence 83, Application US/10491891
; Publication No. US20050059107A1
; GENERAL INFORMATION:
; APPLICANT: MAILLIERE, BERNARD
; APPLICANT: CASTELLI, FLORENCE
; APPLICANT: BUHOT, CECILE
; APPLICANT: GEORGES, BERTRAND
; TITLE OF INVENTION: METHOD OF SELECTING HLA-DP4 LIGANDS AND THE APPLICATIONS THEREOF
; FILE REFERENCE: 251858US0XPCT
; CURRENT APPLICATION NUMBER: US/10/491,891
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: PCT/FR02/03555
; PRIOR FILING DATE: 2002-10-17

; PRIOR APPLICATION NUMBER: FR01/13352
; PRIOR FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-491-891-83

Query Match 100.0%; Score 47; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 9 TVSGNLTIR 18
|||||

RESULT 14
US-10-182-506A-7
; Sequence 7, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-7

Query Match 100.0%; Score 47; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 15 TVSGNLTIR 24
|||||

RESULT 15
US-10-182-506A-6
; Sequence 6, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765

; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-6

Query Match 100.0%; Score 47; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 17 TVSGNLTIR 26
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Search completed: March 13, 2006, 20:02:26
Job time : 61.4706 secs

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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:54:06 ; Search time 6.82353 Seconds
(without alignments)
40.793 Million cell updates/sec

Title: US-09-529-206E-15
Perfect score: 47
Sequence: 1 TVSGNLTIR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
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- 3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 5: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	20	7 US-11-032-498-36	Sequence 36, Appl
2	47	100.0	180	7 US-11-155-288-7	Sequence 7, Appl
3	47	100.0	240	7 US-11-021-441-28	Sequence 28, Appl
4	35	74.5	223	6 US-10-485-517-412	Sequence 412, Appl
5	34	72.3	305	7 US-11-098-686-10549	Sequence 10549, A
6	34	72.3	585	7 US-11-072-512-2739	Sequence 2739, Ap
7	33	70.2	313	7 US-11-190-188-7	Sequence 7, Appl
8	33	70.2	387	6 US-10-467-657-1556	Sequence 1556, Ap
9	33	70.2	426	6 US-10-873-528-34	Sequence 34, Appl
10	33	70.2	471	6 US-10-995-561-901	Sequence 901, Appl
11	33	70.2	517	6 US-10-641-678-47	Sequence 47, Appl
12	32	68.1	105	6 US-10-485-788A-711	Sequence 711, Appl
13	32	68.1	105	7 US-11-053-076-81	Sequence 81, Appl
14	32	68.1	123	6 US-10-467-657-1358	Sequence 1358, Ap
15	32	68.1	523	6 US-10-641-678-45	Sequence 45, Appl
16	31	66.0	92	6 US-10-485-788A-657	Sequence 657, Appl
17	31	66.0	92	7 US-11-053-076-19	Sequence 19, Appl
18	31	66.0	536	6 US-10-641-678-70	Sequence 70, Appl
19	31	66.0	1085	7 US-11-087-099-11646	Sequence 11646, A
20	31	66.0	2204	7 US-11-052-554A-174	Sequence 174, Appl
21	30	63.8	40	6 US-10-895-064-2370	Sequence 2370, Ap
22	30	63.8	194	7 US-11-129-741-2370	Sequence 2370, Ap
23	30	63.8	194	7 US-11-087-099-342	Sequence 342, Appl
24	30	63.8	201	5 US-09-810-501-21	Sequence 21, Appl
25	30	63.8	228	5 US-09-978-360A-516	Sequence 516, Appl

26	30	63.8	280	6 US-10-511-538-41	Sequence 41, Appl
27	30	63.8	319	7 US-11-098-686-11290	Sequence 11290, A
28	30	63.8	340	7 US-11-129-143-43	Sequence 43, Appl
29	30	63.8	350	7 US-11-165-024-3	Sequence 3, Appl
30	30	63.8	353	7 US-11-129-143-55	Sequence 55, Appl
31	30	63.8	359	6 US-10-055-877-159	Sequence 159, Appl
32	30	63.8	406	7 US-11-072-512-3928	Sequence 3928, Ap
33	30	63.8	482	7 US-11-087-099-390	Sequence 390, Appl
34	30	63.8	590	7 US-11-124-368A-183	Sequence 183, Appl
35	30	63.8	590	7 US-11-127-877-54	Sequence 54, Appl
36	30	63.8	668	6 US-10-467-657-5042	Sequence 5042, Ap
37	30	63.8	690	7 US-11-052-554A-232	Sequence 232, Appl
38	29.5	62.8	453	7 US-11-190-188-19	Sequence 19, Appl
39	29	61.7	23	7 US-11-152-366-233	Sequence 233, Appl
40	29	61.7	107	6 US-10-467-657-1054	Sequence 1054, Ap
41	29	61.7	125	6 US-10-467-657-2228	Sequence 2228, Ap
42	29	61.7	135	7 US-11-019-711-86	Sequence 86, Appl
43	29	61.7	155	7 US-11-096-568A-26866	Sequence 26866, A
44	29	61.7	168	7 US-11-087-099-6776	Sequence 6776, Ap
45	29	61.7	201	7 US-11-124-368A-265	Sequence 265, Appl

ALIGNMENTS

RESULT 1
US-11-032-498-36
; Sequence 36, Application US/11032498
; Publication No. US20050249743A1
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Van der Bruggen, Pierre
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-A24 Molecule and Uses Thereof
; FILE REFERENCE: LUD 5881
; CURRENT APPLICATION NUMBER: US/11/032,498
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: US 60/535,751
; PRIOR FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 36
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: NY-ESO-1 peptide
US-11-032-498-36

Query Match 100.0% Score 47; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
| | | | | | | | | |
Db 9 TVSGNLTIR 18

RESULT 2
US-11-155-288-7
; Sequence 7, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MAN/K.050A
; CURRENT APPLICATION NUMBER: US/11/155,288
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-7

Query Match      100.0%; Score 47; DB 7; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TVSGNLTIR 10
Db      127 TVSGNLTIR 136

RESULT 3
US-11-021-441-28
; Sequence 28, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEROOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/615,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein
US-11-021-441-28

Query Match      100.0%; Score 47; DB 7; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TVSGNLTIR 10
Db      187 TVSGNLTIR 196

RESULT 4
US-10-485-517-412
; Sequence 412, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629W0
; CURRENT APPLICATION NUMBER: US/10/485,517
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; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 412
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-485-517-412

Query Match      74.5%; Score 35; DB 6; Length 223;
Best Local Similarity 70.0%; Pred. No. 8.1;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 TVSGNLTIR 10
Db      132 TVGNIMKIR 141

RESULT 5
US-11-098-686-10549
; Sequence 10549, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10549
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10549

Query Match      72.3%; Score 34; DB 7; Length 305;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 VSGNLTIR 10
Db      52 VSGNLTIR 60

RESULT 6
US-11-072-512-2739
; Sequence 2739, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
```

; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cdna
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2739
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2739

Query Match 72.3%; Score 34; DB 7; Length 585;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIT 9
|:|||||
Db 387 TVSGNLTIT 395

RESULT 7

US-11-190-188-7
; Sequence 7, Application US/11190188
; Publication No. US20060035331A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATTERSON, Chandra
; APPLICANT: YAO, Monique G.
; APPLICANT: SHIH, Leo L.
; APPLICANT: TRIBOULEY, Catherine
; APPLICANT: LU, Dying Aina M.
; APPLICANT: YUE, Henry
; APPLICANT: KHAN, Farrah A.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: YANG, Junming
; APPLICANT: HARLAND, Lee
; APPLICANT: WALSH, Roderick T.
; APPLICANT: LO, Terence P.
; APPLICANT: BOROWSKY, Mark L.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0044 PCT
; CURRENT APPLICATION NUMBER: US/11/190,188
; CURRENT FILING DATE: 2005-07-27
; PRIOR APPLICATION NUMBER: US/10/220,382
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,854; 60/190,453; 60/190,730
; PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens

; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 3082743CD1
US-11-190-188-7

Query Match 70.2%; Score 33; DB 7; Length 313;
Best Local Similarity 77.8%; Pred. No. 31;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIT 9
|:|||||
Db 38 TVSGNLTIT 46

RESULT 8

US-10-467-657-1556
; Sequence 1556, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1556
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1556

Query Match 70.2%; Score 33; DB 6; Length 387;
Best Local Similarity 77.8%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 VSGNLTIT 10
|:|||||
Db 77 VSGNLTIT 85

RESULT 9

US-10-873-528-34
; Sequence 34, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1993-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-34

Query Match 70.2%; Score 33; DB 6; Length 426;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIT 9
|:|||||
Db 45 SVAGNLTIT 53

```
RESULT 10
US-10-995-561-901
; Sequence 901, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 901
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-901

Query Match      70.2%; Score 33; DB 6; Length 471;
Best Local Similarity 66.7%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 TVSGNLTIR 9
DB      88 TIAGNLTIR 96

RESULT 11
US-10-641-678-47
; Sequence 47, Application US/10641678
; Publication No. US2005027172A1
; GENERAL INFORMATION:
; APPLICANT: Day, Anthony, G.
; APPLICANT: Goedegebuurt, Frits
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Neefe, Paulien
; APPLICANT: Sandgren, Mats
; APPLICANT: Shaw, Andrew
; APPLICANT: Stahlberg, Jerry
; TITLE OF INVENTION: Novel Variant Hypocrea jecorina CBH1
; FILE REFERENCE: GC772-3
; CURRENT APPLICATION NUMBER: US/10/641,678
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/458,853
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/458,696
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/456,368
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US 60/404,063
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Ipex lacteus
US-10-641-678-47

Query Match      70.2%; Score 33; DB 6; Length 517;
Best Local Similarity 60.0%; Pred. No. 56;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 TVSGNLTIR 10
DB      102 TTSGNLTIR 111

RESULT 12
US-10-485-788A-711
; Sequence 711, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 711
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-711

Query Match      68.1%; Score 32; DB 6; Length 105;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TVSGNLTIR 10
DB      19 TVSGNLTIR 28

RESULT 13
US-11-053-076-81
; Sequence 81, Application US/11053076
; Publication No. US20050255460A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Somoza Diaz-Sarmiento, Chamorro
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008CIP
; CURRENT APPLICATION NUMBER: US/11/053,076
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: PCT/US03/28508
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/490,094
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
```

; SEQ ID NO 81
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-053-076-81

Query Match 68.1%; Score 32; DB 7; Length 105;
Best Local Similarity 80.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 19 TVSGNGLGIR 28

RESULT 14

US-10-467-657-1358
; Sequence 1358, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1358
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1358

Query Match 68.1%; Score 32; DB 6; Length 123;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNIL 7
Db 95 TVSGNVL 101

RESULT 15

US-10-641-678-45
; Sequence 45, Application US/10641678
; Publication No. US20050277172A1
; GENERAL INFORMATION:
; APPLICANT: Day, Anthony, G.
; APPLICANT: Goedegebuur, Frits
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Neefe, Paulien
; APPLICANT: Sandgren, Mats
; APPLICANT: Shaw, Andrew
; APPLICANT: Stahlberg, Jerry
; TITLE OF INVENTION: Novel Variant Hypocrea jecorina CBH1
; FILE REFERENCE: GC772-3
; CURRENT APPLICATION NUMBER: US/10/641,678
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/458,853
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/458,696
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/456,368
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US 60/404,063

; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Ipex lacteus
US-10-641-678-45

Query Match 68.1%; Score 32; DB 6; Length 523;
Best Local Similarity 60.0%; Pred. No. 90;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 102 TTSGNALTIQ 111

Search completed: March 13, 2006, 20:03:29
Job time : 6.82353 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 18:52:59 ; Search time 75.2941 Seconds
(without alignments)
58.355 Million cell updates/sec

Title: US-09-529-206E-25

Perfect score: 55

Sequence: 1 ASGPGGCGAPR 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1980s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	55	100.0	10	2	AAY06015 Human can
2	55	100.0	10	2	AAY05969 Human can
3	55	100.0	10	4	AAB31331 Exemplary
4	55	100.0	10	4	AAB31331 Exemplary
5	55	100.0	10	5	AAB07734 Human MHC
6	55	100.0	10	5	ABg66802 Tumour an
7	55	100.0	10	8	ADG89596 Class I H
8	55	100.0	10	9	ADK08546 Class I H
9	55	100.0	11	2	AAY06068 Human can
10	55	100.0	11	2	AAY06066 Human can
11	55	100.0	12	2	AAY06065 Human can
12	55	100.0	13	2	AAY06064 Human can
13	55	100.0	14	2	AAY05986 Human can
14	55	100.0	15	2	AAY05978 Human can
15	55	100.0	20	2	AAY05979 Human can
16	55	100.0	30	5	AAB05105 Human NYN
17	55	100.0	179	8	ADK68648 Epitope 1
18	55	100.0	180	2	AAB62584 Cancer as
19	55	100.0	180	2	AAB69665 Human NY-
20	55	100.0	180	2	AAY05965 Human can
21	55	100.0	180	3	AAY52430 Human tum
22	55	100.0	180	3	AAY70862 Human oes
23	55	100.0	180	3	AAB03154 Human oes
24	55	100.0	180	4	AAB69946 Human NY-
25	55	100.0	180	4	AAG67164 Amino aci

25	55	100.0	180	4	AAU01535 Human NY-
26	55	100.0	180	4	AAE07714 Human NY
27	55	100.0	180	5	AAU84818 Human NYN
28	55	100.0	180	5	AAU11543 Human tum
29	55	100.0	180	6	ABR58672 Human can
30	55	100.0	180	6	ABR48210 Human bla
31	55	100.0	180	6	ABU56508 Lung can
32	55	100.0	180	6	ABU56508 Lung can
33	55	100.0	180	6	ABU56694 Lung can
34	55	100.0	180	6	ABP74198 Human NY-
35	55	100.0	180	6	ABU64816 Human NY-
36	55	100.0	180	6	ABR83438 Human NY-
37	55	100.0	180	7	ADC09576 NY-ESO-1
38	55	100.0	180	7	ADD35564 Human NY-
39	55	100.0	180	7	ADD35568 Human NY-
40	55	100.0	180	7	ADD25510 Binding d
41	55	100.0	180	7	ADN39068 Cancer/an
42	55	100.0	180	8	ADJ54139 Human NY-
43	55	100.0	180	8	ADM72815 Human NY-
44	55	100.0	180	8	ADM73418 CAG-3 pro
45	55	100.0	180	8	ADM73417 Human NY-
46	55	100.0	180	8	ADQ18451 Human sof

ALIGNMENTS

RESULT 1

AAU06015

ID AAY06015 standard; peptide; 10 AA.

XX

AC AAY06015;

DT 16-AUG-1999 (first entry)

XX

DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.

XX

KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.

XX Homo sapiens.

OS

XX

PN W09918206-A2.

XX

PD 15-APR-1999.

XX

PF 21-SEP-1998; 98WO-US019609.

XX

PR 08-OCT-1997; 97US-0061428P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Wang RF, Rosenberg SA;

XX

DR WPI; 1999-277270/23.

XX

PT Cancer antigen NY ESO1/CAG-3.

XX

PS Example 10; Page 42; 88pp; English.

XX

CC This peptide was identified as an HLA peptide motif following a screen
CC for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see
CC AAX58599). 30 Epitopes (see AAY05988-906017) were identified. The present
CC peptide (ranked 28) corresponds to amino acid residues 53-62 of CAG-1
CC ORF1 (see AAY05965). CAG-1 is a new and potent tumour antigen capable of
CC eliciting an antigen specific immune response by T cells. Cancer peptides
CC (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their
CC variants, are useful as cancer vaccines. A claimed method of preventing
CC or inhibiting cancer involves administering a cancer peptide, with or

CC without an HLA molecule. The cancer peptides form part of, or are derived
 CC from, cancers such as primary or metastatic melanoma, thymoma, lymphoma,
 CC sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
 CC cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
 CC prostate, ovarian, pancreatic and thyroid cancers
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.6; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGAPR 10

DB 1 ASGPGGGAPR 10

RESULT 2

AAY05969

ID AAY05969 standard; peptide; 10 AA.

XX AC AAY05969;

DT 16-AUG-1999 (first entry)

DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine.

XX Homo sapiens.

OS Synthetic.

XX WO9918206-A2.

PN 15-APR-1999.

PD 21-SEP-1998; 98WO-US019609.

PF 08-OCT-1997; 97US-0061428P.

PR (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang RF, Rosenberg SA;

XX WPI; 1999-277270/23.

DR N-PSDB; AAY58600.

XX Cancer antigen NY ESO1/CAG-3.

XX Claim 11; Page 64; 88pp; English.

XX The present sequence represents a cancer peptide that is based on amino
 CC acid residues 55-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965),
 CC a new and potent tumour antigen capable of eliciting an antigen specific
 CC immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-
 CC 3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-
 CC 87), are useful as cancer vaccines that protect against cancer. The
 CC invention provides: vectors and host cells (also useful as vaccines); a
 CC method of diagnosis of cancer or precancer; a transgenic animal;
 CC antiserum oligonucleotides that inhibit expression of the cancer peptide
 CC or tumour antigen; antibodies reacting with a CAG-3 cancer peptide,
 CC useful in diagnostic and detection assays; and methods for preventing or
 CC inhibiting cancer by administering a cancer peptide, with or without an
 CC HLA molecule. The cancer peptides form part of, or are derived from,
 CC cancers such as primary or metastatic melanoma, thymoma, lymphoma,
 CC sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
 CC cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,

CC prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by
 CC inducing cancer-specific T cells in vitro for subsequent return to a
 CC patient
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.6; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGAPR 10

DB 1 ASGPGGGAPR 10

RESULT 3

AAB31331

ID AAB31331 standard; peptide; 10 AA.

XX AC AAB31331;

DT 20-APR-2001 (first entry)

XX Exemplary antigen characteristic of tumours and derived from NY-ESO-1.

XX MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer;

KW MAGE-A1 HLA class II-binding protein; vaccine.

XX Homo sapiens.

XX WO200078806-A1.

PN 28-DEC-2000.

PD 14-JUN-2000; 2000WO-US016287.

PF 18-JUN-1999; 99US-00336091.

PR (LUDW-) LUDWIG INST CANCER RES.

XX Van Snick J, Lethe B, Chaux P, Boon-Falleur T, Van Der Bruggen P;

XX WPI; 2001-102698/11.

XX Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and
 CC are presented to the class II molecules, useful for inducing immune
 CC response and treating cancers characterized by expression of MAGE-A1.
 XX Disclosure; Page 32; 78pp; English.

XX AAB31302-59 represent exemplary antigens which are characteristic of
 CC tumours. They can be used to enhance the immune response of vaccines
 CC comprising peptides derived from human MAGE-A1 HLA (human leukocyte
 CC antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA
 CC binding protein stimulate the activity and proliferation of CD4+ T
 CC lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic
 CC agent for diagnosing a disorder characterized by expression of MAGE-A1.
 CC The protein is used for treating a disorder characterized by expression
 CC of MAGE-A1 such as cancers e.g. melanoma, squamous cell carcinomas,
 CC colorectal carcinomas, osteosarcomas, and lymphocytic leukemias. Peptides
 CC derived from the MAGE-A1 HLA binding protein are useful in the production
 CC of anti-tumour vaccines

XX Sequence 10 AA;

Query Match 100.0%; Score 55; DB 4; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.6; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGAPR 10

DB 1 ASGPGGGAPR 10

```

RESULT 4
AAE07734
ID AAE07734 standard; peptide; 10 AA.
AC
AC AAE07734;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human MHC class I restricted NY ESO-1 cancer peptide #2.
XX
XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
XX class II restricted T cell epitope; MHC-II epitope; cancer antigen;
XX NY ESO-1 protein; CD4+ T lymphocyte; human leukocyte antigen; HLA;
XX tumour-specific humoral-mediated immunity; cancer; cytostatic;
XX immunotherapy.
XX
XX Homo sapiens.
XX
XX WO200155393-A2.
XX
XX 02-AUG-2001.
XX
XX 26-JAN-2001; 2001WO-US002765.
XX
XX 28-JAN-2000; 2000US-0179004P.
XX
XX 29-SEP-2000; 2000US-0237107P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Wang R, Rosenberg SA, Zeng G;
XX
XX WPI; 2001-496851/54.
XX
XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
XX useful as immunogen and vaccine for inhibiting cancer in a mammal or as
XX protection from metastasis.
XX
XX Claim 16; Page 84; 134pp; English.
XX
XX The invention relates to the identification and isolation of major
XX histocompatibility (MHC) class II restricted T cell epitope (MHC-II
XX epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
XX from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leukocyte
XX antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
XX restricted. The products of the gene are promising candidates for
XX immunotherapeutic strategies for the prevention, treatment and diagnosis
XX of patients with cancer. The cancer epitopes are useful as immunogen and
XX vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
XX lymphocytes resulting in protection of the recipient from development of
XX cancer and protection from metastasis, or by inhibiting the growth of
XX cells expressing the NY-ESO-1 gene product. The cancer peptides are also
XX useful as diagnostic agent to detect the presence of cancer, to enhance
XX the generation of antibody and/or CD8+ T cell responses against any given
XX target antigen and/or hapten and to induce tumour-specific humoral-
XX mediated immunity against cancer. The present sequence is MHC class I
XX restricted human NY ESO-1 cancer peptide
XX
XX Sequence 10 AA;
XX
XX Query Match 100.0%; Score 55; DB 4; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.6;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ASGPGGGAPR 10
XX |||||
XX
XX Db 1 ASGPGGGAPR 10
XX
XX RESULT 5
ABG66802
ID ABG66802 standard; peptide; 10 AA.
XX
XX

```

```

AC
XX ABG66802;
XX
XX 24-SEP-2002 (first entry)
XX
XX Tumour antigen NY-ESO-1/CAG3 ORF1, HLA-A31 epitope.
XX
XX Beta-2 microglobulin; beta-2m; cytotoxic T lymphocyte; CTL; HLA;
XX human leukocyte antigen; fusion protein; epitope; cytostatic; tumour;
XX gastrointestinal tumour; colorectal cancer; gastro-oesophageal cancer;
XX liver cancer; biliary tract cancer; pancreatic cancer; vaccine;
XX prostatic cancer; testicular cancer; lung cancer; breast cancer;
XX malignant melanoma; mesothelioma; brain tumour; ovarian cancer;
XX uterine cancer; cervical cancer; head and neck cancer; bladder cancer;
XX Kaposi's sarcoma; renal carcinoma; leukaemia; lymphoma;
XX acquired immunodeficiency syndrome; AIDS-related lymphoma.
XX
XX Homo sapiens.
XX
XX WO200236146-A2.
XX
XX 10-MAY-2002.
XX
XX 01-NOV-2001; 2001WO-GB004844.
XX
XX 02-NOV-2000; 2000GB-00026812.
XX
XX (ISIS-) ISIS INNOVATION LTD.
XX
XX Tafuro S, Meier U, Mcmichael AJ, Bell JI, Layton G, Hunter M;
XX WPI; 2002-508108/54.
XX
XX New polynucleotide capable of expressing an epitope-beta2m fusion protein
XX useful for generating cytotoxic T lymphocyte responses against a tumor
XX and in restoring antigen presentation in the tumor of a host.
XX
XX Disclosure; Page 25; 46pp; English.
XX
XX The invention relates to a new polynucleotide capable of expressing an
XX epitope-beta2m fusion protein useful for generating cytotoxic T
XX lymphocyte (CTL) responses against a tumor or in restoring antigen
XX presentation in the tumor of a host. Also included are a polynucleotide
XX capable of expressing an epitope-beta 2m fusion protein in combination
XX with a vaccination agent that stimulates a CTL response against the
XX epitope of the fusion protein for simultaneous, separate or sequential
XX use in the treatment of cancer and a method of treating a tumor by
XX administering a capable of expressing an epitope-beta 2m fusion protein,
XX and optionally a vaccination agent that stimulates a CTL response against
XX the epitope of the fusion protein. The polynucleotide is useful for
XX generating CTL responses against tumors, for restoring antigen
XX presentation in the tumor, and subsequently for treating cancers, such
XX as gastrointestinal tumour, prostatic, testicular, lung or breast cancer,
XX malignant melanoma, mesothelioma, brain tumour, ovarian cancer, uterine
XX cancer including cervical cancer, cancer of the head and neck, bladder
XX cancer, Kaposi's sarcoma, AIDS (acquired immunodeficiency syndrome) -
XX related, Kaposi's sarcoma, sarcomas, osteosarcoma, renal carcinoma, and
XX haematopoietic malignant tumours such as leukaemia and lymphoma. The
XX epitope is an HLA (human leukocyte antigen) peptide derived from a viral
XX or tumour antigen. The present sequence is a tumour HLA epitope used in
XX the fusion proteins of the invention
XX
XX Sequence 10 AA;
XX
XX Query Match 100.0%; Score 55; DB 5; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.6;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ASGPGGGAPR 10
XX |||||
XX
XX Db 1 ASGPGGGAPR 10
XX
XX RESULT 6

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```

ADG89596
ID  ADG89596 standard; peptide; 10 AA.
XX  AC
XX  ADG89596;
XX  DT
XX  11-MAR-2004 (first entry)
XX  DE
XX  Class I HLA-restricted testis cancer antigen #31.
XX  KW
XX  metastatic cancer cell differentiation; mutated fibronectin;
XX  KW
XX  metastatic cancer; class I HLA-restricted; testis; cancer antigen.
XX  OS
XX  Unidentified.
XX  PN
XX  WO2003100027-A2.
XX  PD
XX  04-DEC-2003.
XX  PF
XX  28-MAY-2003; 2003WO-US016736.
XX  PR
XX  28-MAY-2002; 2002US-0383530P.
XX  PA
XX  (BAYU ) BAYLOR COLLEGE MEDICINE.
XX  PI
XX  Wang R;
XX  WPI; 2004-035134/03.
XX  ID
XX  Identifying a cell that differentiates into a metastatic cancer cell,
XX  PT
XX  useful for preventing metastatic cancer, comprises identifying a mutated
XX  PT
XX  fibronectin in the cell.
XX  PS
XX  Disclosure; SEQ ID NO 39; 137pp; English.
XX  CC
XX  The invention comprises a method for identifying a cell that will
XX  CC
XX  differentiate into a metastatic cancer cell, the method involves
XX  CC
XX  identifying a mutated fibronectin in the cell. The method of the
XX  CC
XX  invention is useful for preventing metastatic cancer. The present amino
XX  CC
XX  acid sequence represents a Class I HLA-restricted testis cancer antigen.
XX  SQ
XX  Sequence 10 AA;
XX  Query Match 100.0%; Score 55; DB 8; Length 10;
XX  Best Local Similarity 100.0%; Pred. No. 0.6;
XX  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  QY
XX  1 ASGPGGGGAPR 10
XX  |||||
XX  1 ASGPGGGGAPR 10
XX  DB
XX  1 ASGPGGGGAPR 10
XX  DE
XX  21-APR-2005 (first entry)
XX  DE
XX  Class I HLA-restricted cancer/testis antigen peptide #31.
XX  KW
XX  vaccine; infection; viral infections; virucide; bacterial infection;
XX  KW
XX  antibacterial; yeast infection; fungicide; fungal infection;
XX  KW
XX  protozoal infection; protozoacide; cancer; cytostatic; melanoma;
XX  KW
XX  lung tumor; colon tumor; breast tumor; leukemia; autoimmune disease;
XX  KW
XX  multiple sclerosis; neuroprotective; rheumatoid arthritis; antiarthritic;
XX  KW
XX  antirheumatic; systemic lupus erythematosus; antiinflammatory;
XX  KW
XX  dermatological; immunosuppressive.
XX  OS
XX  Unidentified.
XX  PN
XX  WO2005011730-A1.
XX  PI
XX  Wang RF, Rosenberg SA;

PD 10-FEB-2005.
XX
XX 30-JUL-2004; 2004WO-GB003285.
XX
XX 01-AUG-2003; 2003GB-00018096.
XX
XX (UNLO ) QUEEN MARY & WESTFIELD COLLEGE.
XX
XX Wang P, Li S;
XX
XX WPI; 2005-152360/16.
XX
XX New vaccine composition comprises inverted microsomes from animal cells
XX PT
XX with an externally disposed peptide antigen and a protein of the Major
XX PT
XX Histocompatibility Complex (MHC), useful for treating or preventing, e.g.
XX PT
XX cancer.
XX
XX Disclosure; Page 48; 83pp; English.
XX
XX The invention comprises a vaccine composition that consists of isolated
XX CC
XX inverted microsomes from an animal cell (or its membrane fragments), in
XX CC
XX association with an externally disposed peptide antigen and a protein of
XX CC
XX the MHC. The vaccine composition of the invention is useful for the
XX CC
XX prophylaxis or treatment of: infection (e.g. viral, bacterial, yeast,
XX CC
XX fungal or protozoal); cancer (e.g. melanoma, lung adenocarcinoma, colon
XX CC
XX cancer, breast cancer or leukemia), autoimmune disease (e.g. multiple
XX CC
XX sclerosis, rheumatoid arthritis or systemic lupus erythematosus). The
XX CC
XX present amino acid sequence represents a class I HLA-restricted cancer
XX CC
XX antigen which was found to be expressed by normal spermatoocytes and/or
XX CC
XX spermatogonia of testis.
XX SQ
XX Sequence 10 AA;
XX Query Match 100.0%; Score 55; DB 9; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.6;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY
XX 1 ASGPGGGGAPR 10
XX 1 ASGPGGGGAPR 10
XX DB
XX 1 ASGPGGGGAPR 10
XX DE
XX 16-AUG-1999 (first entry)
XX DE
XX Human cancer antigen NY ESO-1/CAG-3 peptide.
XX KW
XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
XX KW
XX leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
XX KW
XX metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
XX KW
XX uterine cancer; breast cancer; prostate cancer; ovarian cancer;
XX KW
XX cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
XX KW
XX liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
XX KW
XX vaccine; cytotoxic T lymphocyte; CTL.
XX OS
XX Homo sapiens.
XX
XX WO9918206-A2.
XX
XX 15-APR-1999.
XX
XX 21-SEP-1998; 98WO-US019609.
XX
XX 08-OCT-1997; 97US-0061428P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Wang RF, Rosenberg SA;

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XX WPI; 1999-277270/23.
 XX Cancer antigen NY ESO1/CAG-3.
 PT Example 11; Page 50; 88pp; English.
 XX This peptide corresponds to amino acid residues 53-63 of human NY ESO-1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is capable of eliciting an antigen specific immune response by T cells.
 CC Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers
 XX Sequence 11 AA;
 Query Match 100.0%; Score 55; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.66;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ASGPGGGAPR 10
 |||||
 Db 1 ASGPGGGAPR 10
 RESULT 9
 AAY06066
 ID AAY06066 standard; peptide; 11 AA.
 XX AC AAY06066;
 XX 16-AUG-1999 (first entry)
 XX Human cancer antigen NY ESO-1/CAG-3 peptide.
 DE NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine; cytotoxic T lymphocyte; CTL.
 XX Homo sapiens.
 OS
 XX WO9918206-A2.
 PN
 XX 15-APR-1999.
 PD
 XX 21-SEP-1998; 98WO-US019609.
 PF
 XX 08-OCT-1997; 97US-0061428P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Wang RF, Rosenberg SA;
 PI
 XX WPI; 1999-277270/23.
 DR
 XX Cancer antigen NY ESO1/CAG-3.
 PT
 XX Example 11; Page 50; 88pp; English.
 PS This peptide corresponds to amino acid residues 52-62 of human NY ESO-1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is capable of eliciting an antigen specific immune response by T cells.
 CC Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of

CC preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers
 XX Sequence 11 AA;
 Query Match 100.0%; Score 55; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.66;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ASGPGGGAPR 10
 |||||
 Db 2 ASGPGGGAPR 11
 RESULT 10
 AAY06065
 ID AAY06065 standard; peptide; 12 AA.
 XX AC AAY06065;
 XX 16-AUG-1999 (first entry)
 XX Human cancer antigen NY ESO-1/CAG-3 peptide.
 DE NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine; cytotoxic T lymphocyte; CTL.
 XX Homo sapiens.
 OS
 XX WO9918206-A2.
 PN
 XX 15-APR-1999.
 PD
 XX 21-SEP-1998; 98WO-US019609.
 PF
 XX 08-OCT-1997; 97US-0061428P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Wang RF, Rosenberg SA;
 PI
 XX WPI; 1999-277270/23.
 DR
 XX Cancer antigen NY ESO1/CAG-3.
 PT
 XX Example 11; Page 50; 88pp; English.
 PS This peptide corresponds to amino acid residues 51-62 of human NY ESO-1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is capable of eliciting an antigen specific immune response by T cells.
 CC Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers
 XX Sequence 12 AA;
 Query Match 100.0%; Score 55; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 ASGPGGGAPR 10
Db      3 ASGPGGGAPR 12

RESULT 11
AAY06064
ID      AAY06064 standard; peptide; 13 AA.
XX
AC      AAY06064;
XX
XX      16-AUG-1999 (first entry)
XX
DE      Human cancer antigen NY ESO-1/CAG-3 peptide.
XX
XX      NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW      leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW      metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW      uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW      cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW      liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
XX      vaccine; cytotoxic T lymphocyte; CTL.
XX
OS      Homo sapiens.
XX
XX      WO9918206-A2.
XX
XX      15-APR-1999.
XX
XX      21-SEP-1998; 98WO-US019609.
XX
XX      08-OCT-1997; 97US-0061428P.
XX
XX      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX      Wang RF, Rosenberg SA;
XX      WPI; 1999-277270/23.
XX
XX      Cancer antigen NY ESO1/CAG-3.
XX
XX      Claim 25; Page 50; 88pp; English.
XX
XX      The present sequence represents a cancer peptide that corresponds to
CC      amino acid residues 49-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
CC      AAY05965), a new and potent tumour antigen capable of eliciting an
CC      antigen specific immune response by T cells. Cancer peptides derived from
CC      CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
CC      variants (see AAY05967-87), are useful as cancer vaccines that protect
CC      against cancer. The invention provides: vectors and host cells (also
CC      useful as vaccines); a method of diagnosis of cancer or precancer; a
CC      transgenic animal; antisense oligonucleotides that inhibit expression of
CC      the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
CC      cancer peptide, useful in diagnostic and detection assays; and methods
CC      for preventing or inhibiting cancer by administering a cancer peptide,
CC      with or without an HLA molecule. The cancer peptides form part of, or are
CC      derived from, cancers such as primary or metastatic melanoma, thymoma,
CC      lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
CC      cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
CC      as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
CC      treated by inducing cancer-specific T cells in vitro for subsequent
CC      return to a patient
XX
SQ      Sequence 14 AA;
      Query Match      100.0%; Score 55; DB 2; Length 14;
      Best Local Similarity 100.0%; Pred. No. 0.81;
      Mismatches 0; Indels 0; Gaps 0;
      Matches 10; Conservative 0;

QY      1 ASGPGGGAPR 10
Db      5 ASGPGGGAPR 14

RESULT 13
AAY05978
ID      AAY05978 standard; peptide; 15 AA.
XX
AC      AAY05978;
XX
XX      16-AUG-1999 (first entry)
XX
DE      Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
XX

```

KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO9918206-A2.
 XX
 PD 15-APR-1999.
 XX
 PF 21-SEP-1998; 98WO-US019609.
 XX
 PR 08-OCT-1997; 97US-0061428P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Wang RF, Rosenberg SA;
 XX
 DR WPI; 1999-277270/23.
 XX
 PT Cancer antigen NY ESO1/CAG-3.
 XX
 PS Claim 15; Page 64; 88pp; English.
 XX
 CC The present sequence represents a cancer peptide that corresponds to
 CC amino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
 CC AAY05965), a new and potent tumour antigen capable of eliciting an
 CC antigen specific immune response by T cells. Cancer peptides derived from
 CC CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
 CC variants (see AAY05967-87), are useful as cancer vaccines that protect
 CC against cancer. The invention provides: vectors and host cells (also
 CC useful as vaccines); a method of diagnosis of cancer or precancer; a
 CC transgenic animal; antisense oligonucleotides that inhibit expression of
 CC the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
 CC cancer peptide, useful in diagnostic and detection assays; and methods
 CC for preventing or inhibiting cancer by administering a cancer peptide,
 CC with or without an HLA molecule. The cancer peptides form part of, or are
 CC derived from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
 CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
 CC treated by inducing cancer-specific T cells in vitro for subsequent
 CC return to a patient
 CC
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 55; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.85;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ASGPGGGGAPR 10
 |||||
 Db 6 ASGPGGGGAPR 15
 RESULT 14
 AAY05979
 ID AAY05979 standard; peptide; 20 AA.
 XX
 AC AAY05979;
 XX
 DT 16-AUG-1999 (first entry)
 XX
 DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
 XX
 KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;

KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO9918206-A2.
 XX
 PD 15-APR-1999.
 XX
 PF 21-SEP-1998; 98WO-US019609.
 XX
 PR 08-OCT-1997; 97US-0061428P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Wang RF, Rosenberg SA;
 XX
 DR WPI; 1999-277270/23.
 XX
 PT Cancer antigen NY ESO1/CAG-3.
 XX
 PS Claim 16; Page 64; 88pp; English.
 XX
 CC The present sequence represents a cancer peptide that is based on amino
 CC acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965),
 CC a new and potent tumour antigen capable of eliciting an antigen specific
 CC immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-
 CC 3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-
 CC 87), are useful as cancer vaccines that protect against cancer. The
 CC invention provides: vectors and host cells (also useful as vaccines); a
 CC method of diagnosis of cancer or precancer; a transgenic animal;
 CC antisense oligonucleotides that inhibit expression of the cancer peptide
 CC or tumour antigen; antibodies reacting with a CAG-3 cancer peptide,
 CC useful in diagnostic and detection assays; and methods for preventing or
 CC inhibiting cancer by administering a cancer peptide, with or without an
 CC HLA molecule. The cancer peptides form part of, or are derived from,
 CC cancers such as primary or metastatic melanoma, thymoma, lymphoma,
 CC sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
 CC cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
 CC prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by
 CC inducing cancer-specific T cells in vitro for subsequent return to a
 CC patient
 CC
 XX
 SQ Sequence 20 AA;
 Query Match 100.0%; Score 55; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ASGPGGGGAPR 10
 |||||
 Db 11 ASGPGGGGAPR 20
 RESULT 15
 AAU85105
 ID AAU85105 standard; peptide; 30 AA.
 XX
 AC AAU85105;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human NYNSOla segment 4.
 XX
 KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
 KW viral infection; human immunodeficiency virus; melanoma;
 KW bacterial infection; Salmonella; Legionella; parasitic infection;
 KW Trypanosoma; Toxoplasma; Giardia.
 XX
 OS Homo sapiens.
 XX

PN WO200190197-A1.
XX
PD
XX 29-NOV-2001.
XX
PF 25-MAY-2001; 2001WO-AU000622.
XX
ER 26-MAY-2000; 2000AU-00007761.
XX
FA (AUSU) UNIV AUSTRALIAN NAT.
XX
PI Thomson SA, Ramshaw IA;
XX
XX
WPI: 2002-147575/19.
DR N-PSDB; ABK36925.
DR
XX
PT New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
PS Example 3; Fig 27; 364pp; English.
XX
XX The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention
XX
SQ Sequence 30 AA;
Query Match 100.0%; Score 55; DB 5; Length 30;
Best Local Similarity 100.0%; Pred.No.1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASGPGGGAPR 10
Db |||||
10 ASGPGGGAPR 19
Search completed: March 13, 2006, 19:03:58
Job time : 77.2941 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:04:24 ; Search time 11.8824 Seconds
(without alignments)
80.975 Million cell updates/sec

Title: US-09-529-206E-25

Perfect score: 55

Sequence: 1 ASGPGGGGAPR 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	80.0	3190	2 T13828	CREB-binding prote
2	42	76.4	378	2 C87425	aldose 1-epimerase
3	41	74.5	173	2 AB3648	flagellar basal-bo
4	41	74.5	286	2 S04673	H+-transporting tw
5	41	74.5	357	2 F82878	XAA-PRO aminopepti
6	41	74.5	1207	2 T00378	KIA0641 protein -
7	40	72.7	335	2 S08341	myristylated alani
8	40	72.7	436	2 T36104	conserved hypothet
9	40	72.7	521	2 A29345	steroid hormone re
10	40	72.7	679	2 S02165	regulatory protein
11	40	72.7	954	2 A87431	regulatory protein
12	39	70.9	103	2 C72683	hypothetical prote
13	39	70.9	114	2 B45036	Par beta - human (
14	39	70.9	163	2 B87464	competence/damage-
15	39	70.9	166	2 I69006	histocompatibility
16	39	70.9	187	2 T35619	hypothetical prote
17	39	70.9	260	2 F95899	probable transcrip
18	39	70.9	466	2 F95307	conserved hypothet
19	39	70.9	474	2 G75580	conserved hypothet
20	39	70.9	566	2 T34842	probable transfera
21	39	70.9	575	2 S35327	protein kinase sgg
22	39	70.9	627	2 T35608	polyketide hydroxy
23	39	70.9	733	2 S10932	probable protein k
24	39	70.9	757	2 JC7726	(1->4)-alpha-D-glu
25	39	70.9	1028	2 A56038	DNA-binding protei
26	39	70.9	1067	2 S35423	protein kinase sgg
27	39	70.9	1213	2 S16356	ovo protein - frui
28	39	70.9	1317	2 T03748	apoptosis associat
29	38	69.1	131	2 C75445	pex-related protei

30 38 69.1 161 2 S12246 anther-specific pr
31 38 69.1 189 2 AE3136 Hypothetical Prote
32 38 69.1 189 2 G98151 hypothetical prote
33 38 69.1 201 2 C40040 alternative splici
34 38 69.1 201 2 S26404 alternative splici
35 38 69.1 248 2 A40040 alternative splici
36 38 69.1 286 2 T51008 related to antifir
37 38 69.1 292 2 B40040 alternative splici
38 38 69.1 316 2 AC1965 proline iminoepti
39 38 69.1 327 2 T29031 hypothethical prote
40 38 69.1 331 2 S78452 POU-domain protein
41 38 69.1 341 2 T08459 hypothethical prote
42 38 69.1 341 2 T48847 syntaxin synt4 [im
43 38 69.1 354 2 I80170 class I histocompa
44 38 69.1 397 2 T30168 hypothethical prote
45 38 69.1 420 2 I59234 octamer binding tr

ALIGNMENTS

RESULT 1

T13828

C:Species: Drosophila melanogaster - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T13828

R;Akimaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; G

Nature 386, 735-738, 1997

A;Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling

A;Reference number: Z17785; MUID:97263578; PMID:9109493

A;Accession: T13828

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-3190 <AKI>

A;Cross-references: UNIPROT:O01368; UNIPARC:UPI000003EB83; EMBL:U88570; NID:g1916923; P

C;Genetics:

A;Cross-references: FlyBase:FBgn0015624

A;Map position: X

F;1723-1780/Domain: bromodomain homology <BRO>

Query Match 80.0%; Score 44; DB 2; Length 3190;

Best Local Similarity 77.8%; Pred. No. 1.8e+02;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SGPGGGAPR 10

Db 320 NGPGGGGPR 328

RESULT 2

C87425

aldose 1-epimerase [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: C87425

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J

B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Winn, M.L.; Hart, D.H.; Kolo

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: C87425

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-378 <STO>

A;Cross-references: UNIPROT:Q9A8D6; UNIPARC:UPI00000C73A0; GB:AE005673; NID:g13422779;

C;Genetics:

A;Gene: CC1418

C;Superfamily: aldose 1-epimerase

Query Match 76.4%; Score 42; DB 2; Length 378;

Best Local Similarity 77.8%; Pred. No. 56;

```

Matches      7;  Conservative      1;  Mismatches      1;  Indels      0;  Gaps      0;

QY      2  SGPGGGGAPR 10
      :||| |||||
Db      282  NGPSGGGAPR 290

RESULT 3
AB3648
Flagellar basal-body rod protein flgF [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AB3648
R:DelVecchio, V.G.; Kapratral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A:Reference number: AD3252; PMID:11756688
A:Accession: AB3648
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-173 <KUR>
A:Cross-references: UNIPROT:Q8YA24; UNIPARC:UPI0000058740; GB:AE008918; PIDN:AAL54349.1;
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI1107
A:Map position: II

      Query Match      74.5%;      Score 41;      DB 2;      Length 173;
      Best Local Similarity      100.0%;      Pred. No. 40;
      Matches      7;      Conservative      0;      Mismatches      0;      Indels      0;      Gaps      0;

QY      4  PGGGAPR 10
      |||||
Db      132  PGGGAPR 138

RESULT 4
S04673
H+-transporting two-sector ATPase (BC 3.6.3.14) gamma chain - Rhodopseudomonas blastica
C:Species: Rhodopseudomonas blastica
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 31-Dec-2004
C:Accession: S04673
R:Tybulewicz, V.L.J.; Palk, G.; Walker, J.B.
J. Mol. Biol. 179, 185-214, 1984
A:Title: Rhodopseudomonas blastica atp operon. Nucleotide sequence and transcription.
A:Reference number: S04666; MUID:85058188; PMID:6209404
A:Accession: S04673
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-286 <RYB>
A:Cross-references: UNIPROT:P05436; UNIPARC:UPI0000126582
C:Superfamily: H(+)-transporting ATP synthase gamma chain
C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

      Query Match      74.5%;      Score 41;      DB 2;      Length 286;
      Best Local Similarity      80.0%;      Pred. No. 61;
      Matches      8;      Conservative      0;      Mismatches      2;      Indels      0;      Gaps      0;

QY      1  ASGPGGGGAPR 10
      ||||| |||||
Db      57  ASGQGGGAPR 66

RESULT 5
F82878
XAA-P90 aminopeptidase UUS32 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: F82878
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min

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```

A:Reference number: A82870
A:Accession: F82878
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <GLA>
A:Cross-references: UNIPARC:UPI000000C1CAC; GB:AE002152; GB:AF222894; NID:g6899532; PIDN:
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: pepP; UUS32
A:Genetic code: SGC3
C:Superfamily: X-Pro aminopeptidase

      Query Match      74.5%;      Score 41;      DB 2;      Length 357;
      Best Local Similarity      77.8%;      Pred. No. 74;
      Matches      7;      Conservative      1;      Mismatches      1;      Indels      0;      Gaps      0;

QY      1  ASGPGGGGAP 9
      ||||| |||
Db      193  ASGPNGGSP 201

RESULT 6
T00378
KIAA0641 protein - human
C:Species: Homo sapiens (man)
C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C:Accession: T00378
R:Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N
DNA Res. 5, 169-176, 1998
A:Title: Prediction of the coding sequences of unidentified human genes. X. The complet
A:Reference number: Z14142; MUID:98403880; PMID:9734811
A:Accession: T00378
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1207 <ISH>
A:Cross-references: UNIPARC:UPI0000046CF7; EMBL:AB014541; NID:g3327095; PIDN:BAA31616.1;
C:Genetics:
A:Gene: KIAA0641

      Query Match      74.5%;      Score 41;      DB 2;      Length 1207;
      Best Local Similarity      70.0%;      Pred. No. 2.1e+02;
      Matches      7;      Conservative      1;      Mismatches      2;      Indels      0;      Gaps      0;

QY      1  ASGPGGGGAPR 10
      :||| ||| |||
Db      757  ATGSPGGQPR 766

RESULT 7
S08341
myristylated alanine-rich protein kinase C substrate - bovine
N:Alternate names: acidic calmodulin-binding 81K protein (ACAMP-81); MARCKS
C:Species: Bos primigenius taurus (cattle)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: S08341; A32904; S29270; A46098; PS0338
R:Stumpo, D.J.; Graff, J.M.; Alber, K.A.; Greengard, P.; Blackshear, P.J.
Nucleic Acids Res. 17, 3987-3988, 1989
A:Title: Nucleotide sequence of a cDNA for the bovine myristoylated alanine-rich C kinas
A:Reference number: S08341; MUID:89282412; PMID:2734111
A:Accession: S08341
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-335 <STU>
A:Cross-references: UNIPROT:P12624; UNIPARC:UPI000016C340; EMBL:M24638; NID:g163339; PII
R:Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 4012-4016, 1989
A:Title: Molecular cloning, characterization, and expression of a cDNA encoding the "80-
A:Reference number: A32904; MUID:89264553; PMID:2726763
A:Accession: A32904
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-98,'Q',100-335 <ST2>
A:Cross-references: UNIPARC:UPI000017750A; GB:M24638; GB:M23738

```

R;Herget, T.; Brooks, S.F.; Broad, S.; Rozengurt, E.
 Eur. J. Biochem. 209, 7-14, 1992
 A;Title: Relationship between the major protein kinase C substrates acidic 80-kDa protein or equivalent genes in different species.
 A;Reference number: S29267; MUID:93011168; PMID:1396720
 A;Accession: S29270
 A;Molecule type: DNA
 A;Residues: 191-253; 'SEE', 257-279, 283-292, 'V', 294, 'PEQE', 299, 'A', 300, 'A', 302-313, 'A', 315
 A;Cross-references: UNIPARC:UPI000017750B
 R;Manenti, S.; Sorokine, O.; Van Dorselaer, A.; Taniguchi, H.
 J. Biol. Chem. 268, 6878-6881, 1993
 A;Title: Isolation of the non-myristoylated form of a major substrate of protein kinase C
 A;Reference number: A46098; MUID:93216617; PMID:8463217
 A;Accession: A46098
 A;Molecule type: protein
 A;Residues: 2-11 <MAN>
 A;Cross-references: UNIPARC:UPI000017750C
 R;Mizutani, A.; Tokumitsu, H.; Hidaka, H.
 Biochem. Biophys. Res. Commun. 182, 1395-1401, 1992
 A;Title: Acidic calmodulin binding protein, ACAMP-81, is MARCKS protein interacting with
 A;Reference number: PS0338; MUID:92171958; PMID:1540183
 A;Accession: PS0338
 A;Molecule type: protein
 A;Residues: 12-30; 156-69; 98-98, 'AS', 100-103; 104-109, 'E', 111-123; 156-160; 165-171; 196-215; 251-254
 A;Cross-references: UNIPARC:UPI000017750D; UNIPARC:UPI000017750E; UNIPARC:UPI000017750F; 514
 A;Experimental source: brain
 A;Note: this sequence is identical with that of myristoylated alanine-rich C-kinase substrate
 C;Comment: This protein is a major cellular substrate for protein kinase C and plays a role in calcium signaling.
 C;Genetics:
 A;Introns: 34/3
 C;Superfamily: neurofilament triplet H protein
 C;Keywords: actin binding; blocked amino end; calmodulin binding; lipoprotein; myristylation
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F;158,162,166,169/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 72.7%; Score 40; DB 2; Length 335;
 Best Local Similarity 64.3%; Pred. No. 98;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 1;

Qy 1 ASGPG-----GGAPR 10
 Db 288 AAGPGCPAGGAPR 301
 :||| :|||
 :||| :|||

RESULT 8
 T36104
 conserved hypothetical protein SCE15.01 - Streptomyces coelicolor (fragment)
 C;Species: Streptomyces coelicolor
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: T36104
 R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, April 1999
 A;Reference number: Z21597
 A;Accession: T36104
 A;Status: preliminary; translated from GB/EMBL/DDBB
 A;Molecule type: DNA
 A;Residues: 1-436 <MUR>
 A;Cross-references: UNIPROT:Q8CJX1; UNIPARC:UPI000017AD99; EMBL:AL049707; PIDN:CAB41270.
 A;Experimental source: strain A3(2)
 C;Genetics:
 A;Gene: SCOEDB:SCE15.01

Query Match 72.7%; Score 40; DB 2; Length 436;
 Best Local Similarity 77.8%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASGPGGAP 9
 Db 153 ASGPGGNT 161
 :||| :|||
 :||| :|||

RESULT 11
 A87431
 regulatory protein Flay [imported] - Caulobacter crescentus
 C;Species: Caulobacter crescentus
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C;Accession: A87431
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

RESULT 9

A29345
 steroid hormone receptor ERRL precursor - human
 N;Alternate names: estrogen-related receptor
 C;Species: Homo sapiens (man)
 C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 31-Dec-2004
 C;Accession: A29345; A49074
 R;Giguere, V.; Yang, N.; Segui, P.; Evans, R.M.
 Nature 331, 91-94, 1988
 A;Title: Identification of a new class of steroid hormone receptors.
 A;Reference number: A29345; MUID:88122546; PMID:3267207
 A;Accession: A29345
 A;Molecule type: mRNA
 A;Residues: 1-521 <GIG>
 A;Cross-references: UNIPROT:P11474; UNIPARC:UPI0000142399; EMBL:X51416; NID:g36608; PID
 R;Wiley, S.R.; Kraus, R.J.; Zuo, F.; Murray, E.E.; Loritz, K.; Mertz, J.E.
 Genes Dev. 7, 2206-2219, 1993
 A;Title: SV40 early-to-late switch involves titration of cellular transcriptional repressors.
 A;Reference number: A49074; MUID:94040741; PMID:8224847
 A;Accession: A49074
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 166-169, 'X', 171-173 <WIL>
 A;Cross-references: UNIPARC:UPI000017A1DF
 C;Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; zinc finger
 F;174-434/Domain: erba transforming protein homology <ERBA>
 F;176-196/Region: zinc finger
 F;212-236/Region: zinc finger

Query Match 72.7%; Score 40; DB 2; Length 521;
 Best Local Similarity 77.8%; Pred. No. 1.4e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SGPGGGAPR 10
 Db 465 AGPGGGAER 473
 :||| :|||
 :||| :|||

RESULT 10

S02165
 regulatory protein flay - Caulobacter crescentus
 C;Species: Caulobacter crescentus
 C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
 C;Accession: S02165
 R;Kaplan, J.B.; Dingwall, A.; Bryan, R.; Chamber, R.; Shapiro, L.
 J. Mol. Biol. 205, 71-83, 1989
 A;Title: Temporal regulation and overlap organization of two Caulobacter flagellar gene
 A;Reference number: S02164; MUID:89178645; PMID:2648000
 A;Accession: S02165
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-679 <RAP>
 A;Cross-references: UNIPROT:P15345; UNIPARC:UPI000017A8F7
 C;Genetics:
 A;Gene: flay
 C;Keywords: transcription regulation

Query Match 72.7%; Score 40; DB 2; Length 679;
 Best Local Similarity 77.8%; Pred. No. 1.9e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASGPGGAP 9
 Db 173 AGPGGAGAP 181
 :||| :|||
 :||| :|||

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonin, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: A87431
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-954 <STO>
 A:Cross-references: UNIPROT:P15345; UNIPARC:UPI000012A8ED; GB:AE005673; NID:gl3422833; E
 C:Genetics:
 A:Gene: CC1465

Query Match 72.7%; Score 40; DB 2; Length 954;
 Best Local Similarity 77.8%; Pred. No. 2.4e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASGPGGGAP 9
 |||||
 DB 317 AGPGGAGAP 325

RESULT 12
 C72683

hypothetical protein APE0884 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C:Accession: C72683

A:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix strain K1.
 A:Reference number: A72450; MUID:99310339; PMID:10382966
 A:Accession: C72683
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-103 <KAW>
 A:Cross-references: UNIPROT:Q9YDN0; UNIPARC:UPI000005DD18; DDBJ:AF000060; NID:95104188;
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE0884

Query Match 70.9%; Score 39; DB 2; Length 103;
 Best Local Similarity 85.7%; Pred. No. 49;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GPGGGAP 9
 |||||
 DB 21 GPGGGSP 27

RESULT 13
 B45036

Pur beta - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: B45036
 R:Bergmann, A.D.; Ma, Z.W.; Johnson, E.M. Mol. Cell. Biol. 12, 5673-5682, 1992
 A:Title: Sequence of cDNA comprising the human pur gene and sequence-specific single-strand binding site.
 A:Reference number: B45036; MUID:93078769; PMID:1448097
 A:Accession: B45036
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-114 <BER>
 A:Cross-references: UNIPROT:Q96QR8; UNIPARC:UPI000017C32D
 A:Experimental source: HeLa cells
 A>Note: sequence extracted from NCBI backbone (NCBIP:119218)

Query Match 70.9%; Score 39; DB 2; Length 114;
 Best Local Similarity 87.5%; Pred. No. 54;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASGPGGGA 8
 |||||
 DB 3 AGPGGGA 10

RESULT 14
 E87464

competence/damage-inducible protein ClnA [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 05-Oct-2004
 C:Accession: E87464

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonin, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: E87464
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-163 <STO>
 A:Cross-references: UNIPROT:Q9A7I6; UNIPARC:UPI00000C74AD; GB:AE005673; NID:gl3423155; E
 C:Genetics:
 A:Gene: CC1737

C:Superfamily: uncharacterized protein related to ClnA

Query Match 70.9%; Score 39; DB 2; Length 163;
 Best Local Similarity 75.0%; Pred. No. 73;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SGPGGGAP 9
 :|||||
 DB 106 AGPGGGTP 113

RESULT 15
 I69006

histocompatibility antigen - rhesus macaque (fragment)
 C:Species: Macaca mulatta (rhesus macaque)
 C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
 C:Accession: I69006
 R:Boyson, J.E.; McAdam, S.N.; Gallimore, A.; Golos, T.G.; Liu, X.; Gotch, F.M.; Hughes, Immunogenetics 41, 59-68, 1995
 A:Title: The MHC E locus in macaques is polymorphic and is conserved between macaques and humans.
 A:Reference number: I54551; MUID:95104933; PMID:7806297
 A:Accession: I69006
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-166 <RES>
 A:Cross-references: UNIPROT:Q95518; UNIPARC:UPI0000082D6; EMBL:U02981; NID:9532971; PIR
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Query Match 70.9%; Score 39; DB 2; Length 166;
 Best Local Similarity 77.8%; Pred. No. 74;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 SGPGGGAPR 10
 :|||||
 DB 5 SRPGGGGPR 13

Search completed: March 13, 2006, 19:16:08
 Job time : 13.8824 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 18:53:23 ; Search time 72.5882 Seconds
(without alignments)
97.196 Million cell updates/sec

Title: US-09-529-206B-25
Perfect score: 55
Sequence: 1 ASGPGGGAPR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits, satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_treml.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	142	2	Q9NY13_HUMAN
2	55	100.0	180	1	CTG1B_HUMAN
3	55	100.0	180	2	O7LBY4_HUMAN
4	47	85.5	210	1	CTAG2_HUMAN
5	46	83.6	327	2	Q63HT9_BURPS
6	46	83.6	330	2	Q629N3_BURNA
7	46	83.6	708	2	Q5KJW5_CRYNE
8	46	83.6	708	2	Q5SWM1_CRYNE
9	45	81.8	309	2	Q63N33_BURPS
10	45	81.8	362	2	Q63QT8_BURPS
11	45	81.8	362	2	Q62H22_BURNA
12	45	81.8	788	2	Q4QQP8_HUMAN
13	44	80.0	262	2	Q4NUZ3_9DELT
14	44	80.0	271	2	Q4NAC6_9MICC
15	44	80.0	367	2	Q6AV33_ORYSA
16	44	80.0	398	2	Q8NGH2_HUMAN
17	44	80.0	398	2	Q8NHU1_HUMAN
18	44	80.0	399	2	Q8IVQ3_HUMAN
19	44	80.0	492	2	Q7NWI2_CHRVO
20	44	80.0	566	2	Q5SQT4_HUMAN
21	44	80.0	584	2	Q5P6Z0_AZOSE
22	44	80.0	3190	2	O01368_DROME
23	44	80.0	3276	2	Q9W321_DROME
24	43	78.2	108	2	O8H321_ORYSA
25	43	78.2	218	2	Q69PJ1_ORYSA
26	43	78.2	218	2	Q69PJ3_ORYSA
27	43	78.2	230	2	Q6YPC1_ORYSA
28	43	78.2	270	2	Q6UU54_ORYSA
29	43	78.2	322	2	Q67PU0_SYMTH
30	43	78.2	342	2	Q9SP09_TOBAC
31	43	78.2	392	2	Q6GLG9_XENTR

32	43	78.2	500	2	Q6UU52_ORYSA	O6uu52 oryza sativ
33	43	78.2	560	2	Q4ILQ5_GIBZE	Q4ilq5 gibberella
34	43	78.2	564	2	Q96TZ3_NEUCR	Q96tz3 neurospora
35	43	78.2	571	2	Q4WRL3_ASEPU	Q4wrl3 aspergillus
36	43	78.2	574	2	Q5BEV2_EMENI	Q5bev2 aspergillus
37	43	78.2	640	2	Q6ZV16_HUMAN	Q6zvi6 homo sapien
38	43	78.2	811	2	Q5K4L6_HUMAN	Q5k4l6 homo sapien
39	43	78.2	811	2	Q5VUQ8_HUMAN	Q5vuq8 homo sapien
40	43	78.2	1000	2	Q4FKF7_9TRYP	Q4fkf7 trypanosoma
41	43	78.2	1383	2	Q4SW43_TETNG	Q4sw43 tetraodon n
42	42	76.4	194	2	Q96BU2_HUMAN	Q96bu2 homo sapien
43	42	76.4	217	2	Q4SYU9_TETNG	Q4syu9 tetraodon n
44	42	76.4	344	2	Q4TGY6_TETNG	Q4tgy6 tetraodon n
45	42	76.4	355	2	Q9HBE2_HUMAN	Q9hbe2 homo sapien

ALIGNMENTS

RESULT 1
Q9NY13_HUMAN
ID Q9NY13_HUMAN PRELIMINARY; PRT; 142 AA.
AC Q9NY13;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein LAGE-2 (Fragment).
GN Name=LAGE-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ275978; CAB76945.1; -; mRNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 142 AA; 13895 MW; 27BEB922AC4ACC7B CRC64;

Query Match 100.0%; Score 55; DB 2; Length 142;
Best Local Similarity 100.0%; Pred No. 1.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGAPR 10
|||
DB 27 ASGPGGGAPR 36
|||

RESULT 2
CTG1B_HUMAN
ID CTG1B_HUMAN STANDARD; PRT; 180 AA.
AC P78358;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-ESO-1).
GN Name=CTAG1B; Synonyms=CTAG, CTAG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

QY MEDLINE-97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
Chen Y.-T., Scantlan M.J., Sahin U., Tuereci O., Gure A.O., Tsang S.,
Williamson B., Stockert E., Pfundscht M., Old L.J.;
"A testicular antigen aberrantly expressed in human cancers detected
by autologous antibody screening.";

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EL Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
FN [2]
FP NUCLEOTIDE SEQUENCE.
FC TISSUE=Melanoma;
RX MEDLINE=98289662; PubMed=9626360;
RA Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA de Plaen E., Boon T.;
RT "LAGE-1, a new gene with tumor specificity.";
RL Int. J. Cancer 76:903-908(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98430682; PubMed=9759882;
RA Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,
RA Schwartztruber D.J., Rosenberg S.A.;
RT "A breast and melanoma-shared tumor antigen: T cell responses to
RT antigenic peptides translated from different open reading frames.";
RL J. Immunol. 161:3596-3606(1998).
CC -!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide
CC variety of cancers. Detected in uterine myometrium.
CC -!- SIMILARITY: Belongs to the CTAG family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U87459; AAB49693.1; -; mRNA.
DR EMBL; AJ003149; CAA05908.1; -; mRNA.
DR EMBL; AF038567; RAD05202.1; -; mRNA.
DR HGNC; HGNC:2491; CTAG1B.
DR MIM; 300156; -.
KW Antigen; Transmembrane.
FT TRANSMEM 156 172 Potential.
FT COMPIAS 5' 82 Gly-rich.
SQ SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;

Query Match 100.0%; Score 55; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGAPR 10
DB 53 ASGPGGGAPR 62

RESULT 3
Q7LBY4 HUMAN
ID Q7LBY4 HUMAN PRELIMINARY; PRT; 180 AA.
AC Q7LBY4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
DE antigen 1-B).
GN Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21303268;
RA Galgoczy P., Rosenthal A., Platzer M.;
RT "Human-mouse comparative sequence analysis of the NEMO gene reveals an
RT alternative promoter within the neighboring G6PD gene.";
RL Gene 271:93-98(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21566154; PubMed=11709543; DOI=10.1093/hmg/10.22.2557;
RA Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
RA Patlan H., Ciccedicola A., Kenwick S., Platzer M., D'Urso M.,

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RA Nelson D.L.;
RT "Multiple pathogenic and benign genomic rearrangements occur at a 35
RT kb duplication involving the NEMO and LAGE2 genes.";
RL Hum. Mol. Genet. 10:2557-2567(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Platzer M.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Platzer M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Galgoczy P., Platzer M.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99454989; PubMed=10523621;
RA De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
RT "DNA methylation is the primary silencing mechanism for a set of germ
RT line- and tumor-specific genes with a CpG-rich promoter.";
RL Mol. Cell. Biol. 19:7327-7335(1999).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF277315; AAL27014.1; -; Genomic DNA.
DR EMBL; AJ275977; CAB76943.1; -; Genomic DNA.
DR EMBL; AF277315; AAL27013.1; -; Genomic DNA.
SQ SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGAPR 10
DB 53 ASGPGGGAPR 62

RESULT 4
CTAG2 HUMAN
ID CTAG2 HUMAN STANDARD; PRT; 210 AA.
AC O75638; O75637; Q9UB80; Q9UJ89; Q9Y479;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
GN Name=CTAG2; Synonyms=ESO2, LAGE1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B).
RC TISSUE=Melanoma;
RX MEDLINE=98289662; PubMed=9626360;
RA Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA de Plaen E., Boon T.;
RT "LAGE-1, a new gene with tumor specificity.";
RL Int. J. Cancer 76:903-908(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B), AND VARIANTS
RP GLN-6; GLN-89 AND ARG-138.
RC TISSUE=Melanoma;
RX MEDLINE=99325550; PubMed=10399963;
RA Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT unexpected translation product of LAGE-1.";
RL Int. J. Cancer 82:442-448(1999).
RN [3]

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Qy		1	ASGPGGGAPR 10 53 ASGPRGGAPR 62	
Db				
RESULT 5				
Q63HT9_BURPS				
ID	Q63HT9_BURPS PRELIMINARY;	PRT;	327 AA.	
AC	Q63HT9;			
DT	25-OCT-2004 (TrEMBLrel. 28, Created)			
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)			
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)			
DE	Putative lipoprotein.			
GN	OrderedLocusNames=BPSS2331;			
OS	Burkholderia pseudomallei [Pseudomonas pseudomallei]			
OC	Bacteria; Proteobacteria; Betaproteobacteriales; Burkholderiales;			
OC	Burkholderiaceae; Burkholderia; pseudomallei group.			
OX	NBUI_TaxID=28450;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=K96243;			
RX	PubMed=15377794; DOI=10.1073/pnas.0403302101;			
RA	Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,			
RA	Ackins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,			
RA	Bentley S.D., Sebailha M., Thomson N.R., Bason N., Beacham I.R.,			
RA	Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,			
RA	Chillingworth T., Cronin A., Crossett B., Davis P., Deshazer D.,			
RA	Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jageles K.,			
RA	Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,			
RA	Rabbinowitz E., Ruthvenford K., Sanders M., Simmonds M.,			
RA	Songjivilai S., Stevens K., Tumapa S., Vesaratchavest M.,			
RA	Whitehead S., Yeats C., Barrell B.G., Oyston P.C.P., Parkhill J.;			
RT	"Genomic plasticity of the causative agent of melioidosis,			
RT	Burkholderia pseudomallei.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).			
DR	EMBL; BX571966; CAH39817.1; -; Genomic_DNA.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	InterPro; IPR007428; VacJ.			
DR	PFam; PF04333; VacJ; 1			
DR	PRINTS; PR01805; VACLIPOPROT.			
KW	Complete proteome; Lipoprotein.			
SQ	SEQUENCE 327 AA; 33687 MW; ACSD2C7CC4A44A25 CRC64;			
	Query Match 83.6%; Score 46; DB 2; Length 327;			
	Best Local Similarity 88.9%; Pred No. 78;			
	Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps			
Qy		1	ASGPGGGAP 9 243 AGGPGGGAP 251	
Db				
RESULT 6				
G629N3_BURMA				
ID	G629N3_BURMA PRELIMINARY;	PRT;	330 AA.	
AC	G629N3;			
DT	25-OCT-2004 (TrEMBLrel. 28, Created)			
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)			
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)			
DE	Putative lipoprotein.			
GN	OrderedLocusNames=BMAA2092;			
OS	Burkholderia mallei (Pseudomonas mallei).			
OC	Bacteria; Proteobacteria; Betaproteobacteriales; Burkholderiales;			
OC	Burkholderiaceae; Burkholderia.			
OX	NBUI_TaxID=13373;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=ATCC 23344;			
RX	PubMed=15377793; DOI=10.1073/pnas.0403306101;			
RA	Nierman W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E.,			
RA	Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,			
RA	Davidson S.C., Davidsen T.D., DeBoy R.T., Dmitrov G., Dodson R.J.,			

RA Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
 FA Madupu R., Mohammad Y., Nelson W.C., Radune D., Romero C.M.,
 FA Sarria S., Seliengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
 FA Zafar N., Zhou L., Fraser C.M.;
 FT "Structural flexibility in the Burkholderia mallei genome.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251 (2004).
 DR EMBL; CP000011; AAU47030.1; -, Genomic_DNA.
 DR TIGR; BAA2092; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR007428; VacJ.
 DR Pfam; PF04333; VacJ; 1.
 DR PRINTS; PR01805; VACJLIPOPROT.
 KW Complete proteome; Lipoprotein.
 SQ SEQUENCE 330 AA; 33977 MW; 2F12165CD7366835 CRC64;

 Query Match 83.6%; Score 46; DB 2; Length 330;
 Best Local Similarity 88.9%; Pred. No. 78;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 ASGPGGGAP 9
 DB 243 AGGPGGGAP 251

 RESULT 7
 Q5KJMS CRYNE
 ID Q5KJMS CRYNE PRELIMINARY; PRT; 708 AA.
 AC Q5KJMS;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Actin cross-linking, putative.
 GN ORFNames=CNC06000;
 OS Cryptococcus neoformans var. neoformans JEC21.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 OX NCBI_TaxID=214684;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=JEC21;
 RA Loftus B., Miranda M., Rongaglia P., Vamathevan J., Utterback T.,
 RA Van Aken S., Fraser C.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBSJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=JEC21;
 RX PubMed=15653466; DOI=10.1126/science.1103773;
 RA Loftus B.J., Funf E., Rongaglia P., Rowley D., Amedeo P., Bruno D.,
 RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
 RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
 RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
 RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
 RA Kwon-Chung K.J., Lenceller K.B., Maiti R., Marra M.A., Marra R.E.,
 RA Mathewson C.A., Mitchell T.G., Pettea M., Riggs F.R., Salzberg S.L.,
 RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
 RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
 RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
 RA Fraser C.M., Hyman R.W.;
 RT "The genome of the basidiomycetous yeast and human pathogen
 Cryptococcus neoformans.";
 RL Science 307:1321-1324 (2005).
 DR EMBL; AE017343; AAU42672.1; -, Genomic_DNA.
 DR GO; GO:0003779; F:actin binding; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR001589; Actnin actin bd.
 DR InterPro; IPR001715; Calponin act bd.
 DR InterPro; IPR011992; EF-Hand Type.
 DR InterPro; IPR002017; Spectrin.
 DR Pfam; PF00307; CH; 2.
 DR SMART; SM00033; CH; 2.
 DR PROSITE; PS00019; ACTININ_1; UNKNOWN_1.
 DR PROSITE; PS00020; ACTININ_2; 1.
 DR PROSITE; PS50021; CH; 2.

KW Complete proteome.
 SQ SEQUENCE 708 AA; 79873 MW; BAF52D1DD2C99B9D CRC64;

 Query Match 83.6%; Score 46; DB 2; Length 708;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 ASGPGGGAP 9
 DB 47 AGGPGGGAP 55

 RESULT 8
 Q55WMI CRYNE
 ID Q55WMI CRYNE PRELIMINARY; PRT; 708 AA.
 AC Q55WMI;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=CNC1180;
 OS Cryptococcus neoformans var. neoformans B-3501A.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
 OX NCBI_TaxID=283643;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B-3501A;
 RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
 RA Wickes B.L., Fu J., Davis R.W.;
 RT "Cryptococcus neoformans serotype D sequencing.";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBSJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AAEY01000013; EAL21978.1; -, Genomic DNA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR InterPro; IPR001589; Actnin actin bd.
 DR InterPro; IPR001715; Calponin act bd.
 DR InterPro; IPR002017; EF-Hand Type.
 DR Pfam; PF00307; CH; 2.
 DR SMART; SM00033; CH; 2.
 DR PROSITE; PS00019; ACTININ_1; UNKNOWN_1.
 DR PROSITE; PS00020; ACTININ_2; UNKNOWN_1.
 DR PROSITE; PS50021; CH; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 708 AA; 79873 MW; BAF52D1DD2C99B9D CRC64;

 Query Match 83.6%; Score 46; DB 2; Length 708;
 Best Local Similarity 88.9%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 ASGPGGGAP 9
 DB 47 AGGPGGGAP 55

 RESULT 9
 Q63N33 BURPS
 ID Q63N33 BURPS PRELIMINARY; PRT; 309 AA.
 AC Q63N33;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Putrescine transport system permease protein.
 GN Name=pot1; OrderedLocaNames=BPS00464;
 OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia; pseudomallei group.
 OX NCBI_TaxID=28450;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.


```

RC STRAIN=K96243; DOI=10.1073/pnas.0403302101;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdano-Tarraga A.-M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosssett B., Davis P., DeShazer D.,
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RL Burkholderia pseudomallei."
CC -!- FUNCTION: Part of a binding-protein-dependent transport system.
CC the membrane (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family.
CC EMBL: BX571966; CAH37920.1; -; Genomic DNA.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0016020; C: membrane; IEA.
DR GO: GO:0005215; F: transporter activity; IEA.
DR GO: GO:0006810; P: transport; IEA.
DR InterPro: IPR000515; BPD transp.; IEA.
DR Pfam: PF00528; BPD transp_1; I.
DR PROSITE: PS00928; ABC_TM1; I.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 309 AA; 33544 MW; 379E21B5B31CDE30 CRC64;

Query Match 81.8%; Score 45; DB 2; Length 309;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SGPGGGAPR 10
||| |||||
DB 287 SGPAGGAPR 295

RESULT 10
Q63Q78_BURPS
ID Q63Q78_BURPS PRELIMINARY; PRT; 362 AA.
AC Q63Q78;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Putative DNA polymerase III.
GN OrderedLocusNames=BPSL2936;
OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; pseudomallei group.
OX NCBI_TaxID=28450;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K96243; DOI=10.1073/pnas.0403302101;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdano-Tarraga A.-M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosssett B., Davis P., DeShazer D.,
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RL Burkholderia pseudomallei."
CC -!- FUNCTION: Part of a binding-protein-dependent transport system.
CC the membrane (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family.
CC EMBL: BX571966; CAH37920.1; -; Genomic DNA.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0016020; C: membrane; IEA.
DR GO: GO:0005215; F: transporter activity; IEA.
DR GO: GO:0006810; P: transport; IEA.
DR InterPro: IPR000515; BPD transp.; IEA.
DR Pfam: PF00528; BPD transp_1; I.
DR PROSITE: PS00928; ABC_TM1; I.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 309 AA; 33544 MW; 379E21B5B31CDE30 CRC64;

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DR GO: GO:0006260; P: DNA replication; IEA.
DR InterPro: IPR010372; DNA_pol3_delta.
DR InterPro: IPR005790; DNA_polIII_delta.
DR Pfam: PF06144; DNA_pol3_delta; I.
DR TIGRFAMs: TIGR01128; hola; I.
KW Complete proteome.
SQ SEQUENCE 362 AA; 38726 MW; D5FF3DE783D41E41 CRC64;

Query Match 81.8%; Score 45; DB 2; Length 362;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASGPGGGAPR 10
||| |||||
DB 350 AAGPGGDAPR 359

RESULT 11
Q62H22_BURMA
ID Q62H22_BURMA PRELIMINARY; PRT; 362 AA.
AC Q62H22;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE DNA polymerase III, delta subunit (EC 2.7.7.7).
GN Name=hola; OrderedLocusNames=BMA2451;
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=13373;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 23344; DOI=10.1073/pnas.0403306101;
RA Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA Daugherty S.C., Davidse T.D., DeBoy R.T., Dmitrov G., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA Madupu R., Mohammud Y., Nelson W.C., Radune D., Romero C.M.,
RA Sarria S., Selengut J., Shambhlin C., Sullivan S.A., White O., Yu Y.,
RA Zafar N., Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome."
RL Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR EMBL: CP000010; AAU49707.1; -; Genomic DNA.
DR TIGR: BMA2451; -;
DR GO: GO:0003887; F: DNA-directed DNA polymerase activity; IEA.
DR GO: GO:0016740; F: transferase activity; IEA.
DR GO: GO:0006260; P: DNA replication; IEA.
DR InterPro: IPR010372; DNA_pol3_delta.
DR InterPro: IPR005790; DNA_polIII_delta.
DR Pfam: PF06144; DNA_pol3_delta; I.
DR TIGRFAMs: TIGR01128; hola; I.
KW Complete proteome; Nucleotidyltransferase; Transferase.
SQ SEQUENCE 362 AA; 38726 MW; D5FF3DE783D41E41 CRC64;

Query Match 81.8%; Score 45; DB 2; Length 362;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASGPGGGAPR 10
||| |||||
DB 350 AAGPGGDAPR 359

RESULT 12
Q4QQP8_HUMAN
ID Q4QQP8_HUMAN PRELIMINARY; PRT; 788 AA.
AC Q4QQP8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE PTGFRN protein (Fragment).
GN Name=PTGFRN;

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
RN [1]_TaxID=9606;
RX NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeng B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.F., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC098142; AAH98142.1; -; mRNA.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR Pfam: PF00047; IG; 2.
DR SMART: SM00409; IG; 5.
DR PROSITE: PS08335; IG LIKE; 4.
FT NON TER 1
SQ SEQUENCE 788 AA; 88279 MW; F49E034EE2D3603B CRC64;

Query Match 81.8%; Score 45; DB 2; Length 788;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASGGGGGAP 9
Db | | | | | | | | | |

RESULT 13
Q4NUZ3_9DELTT
ID Q4NUZ3_9DELTT PRELIMINARY; PRT; 262 AA.
AC Q4NUZ3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Translation initiation factor 2.
GN ORFNames=AdchDRAFT_2230;
OS Anaeromyxobacter dehalogenans 2CP-C.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cytophactereae; Myxococcaceae; Anaeromyxobacter.
OX NCBI_TaxID=290397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Anaeromyxobacter
RT dehalogenans 2CP-C.";

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RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Anaeromyxobacter
RT dehalogenans 2CP-C.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAH01000012; EAL79408.1; -; Genomic_DNA.
KW Initiation factor.
SQ SEQUENCE 262 AA; 25294 MW; 7EF93CC8DE0B47FF CRC64;

Query Match 80.0%; Score 44; DB 2; Length 262;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GPGGGAPR 10
Db | | | | | | | | | |

RESULT 14
Q4NAC6_9MICC
ID Q4NAC6_9MICC PRELIMINARY; PRT; 271 AA.
AC Q4NAC6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=ArthDRAFT_0388;
OS Arthrobacter sp. FB24.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococccineae; Micrococcaceae; Arthrobacter.
OX NCBI_TaxID=290399;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Arthrobacter sp. FB24.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FB24;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Arthrobacter sp. FB24.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAH01000033; EAL94269.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 271 AA; 29989 MW; 5ECC048B06CDD5BA CRC64;

Query Match 80.0%; Score 44; DB 2; Length 271;
Best Local Similarity 87.5%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GPGGGAPR 10
Db | | | | | | | | | |

RESULT 15
Q6AV33_ORYSA
ID Q6AV33_ORYSA PRELIMINARY; PRT; 367 AA.
AC Q6AV33;

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DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein OSJNBa0063J18.9.
 GN Name=OSJNBa0063J18.9;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
 RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
 RA Fadrosch D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
 RA Vanaken S.S., Riedmuller S.B., Uterback T.T., Feldblyum T.V.,
 RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
 RA White O., Salzberg S.L., Fraser C.M.;
 RT "Oryza sativa chromosome 3 BAC OSJNBa0063J18 genomic sequence.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC107206; AAT77052.1; -; Genomic_DNA.
 DR Gramene; Q6AV33; -;
 KW Hypothetical protein.
 SQ SEQUENCE 367 AA; 37474 MW; B8C62D9D4CC18C86 CRC64;

Query Match 80.0%; Score 44; DB 2; Length 367;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASGFGGAPR 10
 DB 94 ASGFGGGSAR 103

Search completed: March 13, 2006, 19:14:23
 Job time : 74.5882 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:14:49 ; Search time 18.5882 Seconds
(without alignments)
44.477 Million cell updates/sec

Title: US-09-529-206E-25

Perfect score: 55

Sequence: 1 ASGPGGAPR 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Issued Patents AA:*
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3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCRU COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	180	1	US-08-791-495-9
2	55	100.0	180	2	US-08-937-263B-8
3	55	100.0	180	2	US-09-751-798-8
4	55	100.0	180	2	US-09-392-714-25
5	55	100.0	180	2	US-09-165-546B-15
6	55	100.0	180	2	US-09-341-829A-9
7	55	100.0	180	2	US-09-849-602-30
8	47	85.5	180	1	US-08-791-495-7
9	47	85.5	180	2	US-09-341-829A-7
10	47	85.5	210	1	US-08-791-495-5
11	47	85.5	210	2	US-09-341-829A-5
12	45	81.8	421	2	US-09-252-991A-32326
13	43	78.2	9	2	US-09-344-040C-117
14	43	78.2	9	2	US-09-833-039A-117
15	43	78.2	210	2	US-09-252-991A-24923
16	43	78.2	809	2	US-09-252-991A-31759
17	42	76.4	160	2	US-09-252-991A-17249
18	42	76.4	283	2	US-09-252-991A-17831
19	42	76.4	836	2	US-09-491-356C-21
20	42	76.4	1427	2	US-09-252-991A-20577
21	41	74.5	143	2	US-08-789-329C-10
22	41	74.5	172	2	US-08-789-329C-7
23	41	74.5	175	2	US-08-789-329C-3
24	41	74.5	340	2	US-09-949-002-562
25	41	74.5	412	1	US-08-878-989-6
26	41	74.5	412	2	US-09-272-796-6
27	41	74.5	536	2	US-09-270-767-43766

28 41 74.5 555 2 US-10-104-047-3369 Sequence 3369, Ap
29 41 74.5 679 2 US-09-252-991A-27111 Sequence 27111, A
30 41 74.5 807 2 US-09-252-991A-32992 Sequence 32992, A
31 41 74.5 1000 2 US-09-252-991A-31361 Sequence 31361, A
32 41 74.5 1207 2 US-10-098-600B-16 Sequence 16, Appl
33 41 74.5 1207 2 US-09-949-002-376 Sequence 376, Appl
34 41 74.5 1323 2 US-09-248-796A-19543 Sequence 19543, A
35 41 74.5 1384 2 US-08-976-255-11 Sequence 11, Appl
36 40 72.7 137 2 US-09-252-991A-20489 Sequence 20489, A
37 40 72.7 174 2 US-09-902-540-12423 Sequence 12423, A
38 40 72.7 291 2 US-09-902-540-15052 Sequence 15052, A
39 40 72.7 335 1 US-08-405-175A-6 Sequence 6, Appli
40 40 72.7 424 2 US-09-252-991A-20642 Sequence 20642, A
41 40 72.7 438 2 US-09-949-016-7812 Sequence 7812, Ap
42 40 72.7 502 2 US-10-088-045-2 Sequence 2, Appli
43 40 72.7 502 2 US-10-088-045-4 Sequence 4, Appli
44 40 72.7 505 1 US-08-660-765A-2 Sequence 2, Appli
45 40 72.7 518 1 US-08-836-620A-18 Sequence 18, Appli

ALIGNMENTS

RESULT 1

US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth , Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Fallieur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 55; DB 1; Length 180;

Best Local Similarity 100.0%; Pred. No. 2.7; 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0;

QY 1 ASGPGGAPR 10

Db 53 ASGPGGAPR 62

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RESULT 2
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Driifhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; FILING DATE: September 15, 1997
; PRIOR APPLICATION NUMBER: US/08/937,263B
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-08-937-263B-8

Query Match 100.0%; Score 55; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGAPR 10
Db 53 ASGPGGGAPR 62

RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
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; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; FILING DATE:
; PRIOR APPLICATION NUMBER: US/09/751,798
; FILING DATE:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6525177man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-09-751-798-8

Query Match 100.0%; Score 55; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGAPR 10
Db 53 ASGPGGGAPR 62

RESULT 4
US-09-392-714-25
; Sequence 25, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-392-714-25

Query Match 100.0%; Score 55; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGAPR 10
Db 53 ASGPGGGAPR 62
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RESULT 5
US-09-165-546D-15
; Sequence 15, Application US/09165546D
; Patent No. 6723832
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
;           Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                   SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CH
;                   USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546D
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6723832man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15

Query Match 100.0%; Score 55; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGGAPR 10
Db 53 ASGPGGGGAPR 62

RESULT 6
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; <151> 1997-01-27

Query Match 100.0%; Score 55; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGGAPR 10
Db 53 ASGPGGGGAPR 62

RESULT 7
US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30

Query Match 100.0%; Score 55; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGGAPR 10
Db 53 ASGPGGGGAPR 62

RESULT 8
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-495-7

Query Match      85.5%; Score 47; DB 1; Length 180;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ASGPGGGGAPR 10
      ||||| |||||
Db      53 ASGPRGGGAPR 62

RESULT 9
US-09-341-829A-7
; Sequence 7, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-341-829A-7

Query Match      85.5%; Score 47; DB 2; Length 180;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ASGPGGGGAPR 10
      ||||| |||||
Db      53 ASGPRGGGAPR 62

RESULT 10
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

; APPLICATION NUMBER: US/08/791,495
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-495-5

Query Match      85.5%; Score 47; DB 1; Length 210;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ASGPGGGGAPR 10
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Db      53 ASGPRGGGAPR 62

RESULT 11
US-09-341-829A-5
; Sequence 5, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-341-829A-5

Query Match      85.5%; Score 47; DB 2; Length 210;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ASGPGGGGAPR 10
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Db      53 ASGPRGGGAPR 62

RESULT 12
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US-09-252-991A-32326
; Sequence 32326, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32326
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32326

Query Match 81.8%; Score 45; DB 2; Length 421;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASGPGGGGAP 9
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Db 358 APGPGGGAP 366

RESULT 13
US-09-344-040C-117
; Sequence 117, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining Expression of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 117
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-117

Query Match 78.2%; Score 43; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGGA 8
| | | | | | | | | |
Db 2 ASGPGGGGA 9

RESULT 14
US-09-833-039A-117
; Sequence 117, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur

; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 117
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-117

Query Match 78.2%; Score 43; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGGA 8
| | | | | | | | | |
Db 2 ASGPGGGGA 9

RESULT 15
US-09-252-991A-24923
; Sequence 24923, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24923
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24923

Query Match 78.2%; Score 43; DB 2; Length 210;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASGPGGGGAPR 10
| | | | | | | | | |
Db 161 ADGAGGGAPR 170

Search completed: March 13, 2006, 19:18:50
Job time : 19.5882 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:51:56 ; Search time 60.4706 Seconds
(without alignments)
69.096 Million cell updates/sec

Title: US-09-529-206E-25
Perfect score: 55
Sequence: 1 ASGPGGGAPR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	4	US-10-447-161-39
2	55	100.0	10	4	US-10-415-841A-52
3	55	100.0	10	5	US-10-182-506A-23
4	55	100.0	30	4	US-10-296-734-1404
5	55	100.0	179	5	US-10-482-029-202
6	55	100.0	180	3	US-09-751-798-8
7	55	100.0	180	3	US-09-849-602-30
8	55	100.0	180	4	US-10-023-182-8
9	55	100.0	180	4	US-10-207-655-71
10	55	100.0	180	4	US-10-364-614-14
11	55	100.0	180	4	US-10-026-066-3
12	55	100.0	180	4	US-10-117-937-74
13	55	100.0	180	4	US-10-295-027-386
14	55	100.0	180	4	US-10-296-734-832
15	55	100.0	180	4	US-10-188-832-139
16	55	100.0	180	4	US-10-777-053-11
17	55	100.0	180	4	US-10-751-088-15
18	55	100.0	180	4	US-10-657-022-74
19	55	100.0	180	4	US-10-837-217-11
20	55	100.0	180	5	US-10-877-373-9
21	55	100.0	180	5	US-10-723-860-1270
22	55	100.0	180	5	US-10-871-708-7
23	55	100.0	180	5	US-10-895-523-3
24	55	100.0	180	5	US-10-182-506A-3
25	55	100.0	180	5	US-10-756-149-5024
26	55	100.0	180	6	US-11-067-064-74
27	55	100.0	180	6	US-11-067-159-74

28	55	100.0	397	3	US-09-821-883-27	Sequence 27, Appl
29	55	100.0	397	6	US-11-144-912-27	Sequence 27, Appl
30	55	100.0	3541	4	US-10-296-734-1454	Sequence 1454, Ap
31	47	85.5	30	4	US-10-296-734-1436	Sequence 1436, Ap
32	47	85.5	135	4	US-10-295-027-388	Sequence 388, App
33	47	85.5	135	4	US-10-188-832-141	Sequence 141, App
34	47	85.5	180	4	US-10-146-473-69	Sequence 69, Appl
35	47	85.5	180	4	US-10-117-937-75	Sequence 75, Appl
36	47	85.5	180	4	US-10-296-734-834	Sequence 834, App
37	47	85.5	180	4	US-10-468-406-4	Sequence 4, Appl
38	47	85.5	180	4	US-10-657-022-75	Sequence 75, Appl
39	47	85.5	180	5	US-10-877-373-7	Sequence 7, Appl
40	47	85.5	180	6	US-11-067-064-75	Sequence 75, Appl
41	47	85.5	180	6	US-11-067-159-75	Sequence 75, Appl
42	47	85.5	210	4	US-10-157-031-88	Sequence 88, Appl
43	47	85.5	210	4	US-10-117-937-76	Sequence 76, Appl
44	47	85.5	210	4	US-10-657-022-76	Sequence 76, Appl
45	47	85.5	210	5	US-10-877-373-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-10-447-161-39
; Sequence 39, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-39

Query Match 100.0%; Score 55; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASGPGGGAPR 10
Db 1 ASGPGGGAPR 10

RESULT 2
US-10-415-841A-52
; Sequence 52, Application US/10415841A
; Publication No. US20040131598A1
; GENERAL INFORMATION:
; APPLICANT: Tafuro, Sabrina
; APPLICANT: Meier, Ute-Christiane
; APPLICANT: McMichael, Andrew James
; APPLICANT: Bell, John Irving
; APPLICANT: Layton, Guy
; APPLICANT: Hunter, Michael
; TITLE OF INVENTION: Cancer Therapy
; FILE REFERENCE: 3547.1001-000
; CURRENT APPLICATION NUMBER: US/10/415,841A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: PCT/GB01/04844
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 52
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-841A-52

Query Match      100.0%; Score 55; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ASGPGGGGAPR 10
      |||||
Db      1 ASGPGGGGAPR 10

RESULT 3
US-10-182-506A-23
; Sequence 23, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; TITLE OF INVENTION: ANTIGEN, NY ESO-1
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-23

Query Match      100.0%; Score 55; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ASGPGGGGAPR 10
      |||||
Db      1 ASGPGGGGAPR 10

RESULT 4
US-10-296-734-1404
; Sequence 1404, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramehew, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1404
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
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; OTHER INFORMATION: NYSO1a segment 4
US-10-296-734-1404

Query Match      100.0%; Score 55; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ASGPGGGGAPR 10
      |||||
Db      10 ASGPGGGGAPR 19

RESULT 5
US-10-482-029-202
; Sequence 202, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-202

Query Match      100.0%; Score 55; DB 5; Length 179;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ASGPGGGGAPR 10
      |||||
Db      53 ASGPGGGGAPR 62

RESULT 6
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. US2002010321A1
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseing; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
```


; APPLICANT: KNUTH, Alexander
; APPLICANT: OLD, Lloyd
; APPLICANT: Gnjatich, Sacha
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
; FILE REFERENCE: LUD 5726.1 CIP
; CURRENT APPLICATION NUMBER: US/10/364,614
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/355,828
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-614-14

Query Match 100.0%; Score 55; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGAPR 10
Db 53 ASGPGGGAPR 62

RESULT 11
US-10-026-066-3
; Sequence 3, Application US/10026066
; Publication No. US20030215425A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
; FILE REFERENCE: CTLIMM-21CP1C
; CURRENT APPLICATION NUMBER: US/10/026,066
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-026-066-3

Query Match 100.0%; Score 55; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGAPR 10
Db 53 ASGPGGGAPR 62

RESULT 12
US-10-117-937-74
; Sequence 74, Application US/10117937
; Publication No. US2003020239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.

; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-74

Query Match 100.0%; Score 55; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGAPR 10
Db 53 ASGPGGGAPR 62

RESULT 13
US-10-295-027-386
; Sequence 386, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 386

; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-386

Query Match 100.0%; Score 55; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGAPR 10
| | | | | | | | | |
Db 53 ASGPGGGAPR 62

RESULT 14

US-10-296-734-832
; Sequence 832, Application US/10296734
; Publication No. US20040054137A1

; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU P07761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 832
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYNsola consensus polypeptide
US-10-296-734-832

Query Match 100.0%; Score 55; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGAPR 10
| | | | | | | | | |
Db 53 ASGPGGGAPR 62

RESULT 15

US-10-188-832-139
; Sequence 139, Application US/10188832
; Publication No. US20040076955A1

; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139

; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-139

Query Match 100.0%; Score 55; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGAPR 10
| | | | | | | | | |
Db 53 ASGPGGGAPR 62

Search completed: March 13, 2006, 20:02:26
Job time : 60.4706 secs

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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:54:06 ; Search time 6.82353 Seconds
(without alignments)
40.793 Million cell updates/sec

Title: US-09-529-206E-25

Perfect score: 55

Sequence: 1 ASGPGGGAPR 10

Scoring table: BLOSUM62

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Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA_New:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	55	100.0	180	7	US-11-155-288-7
2	55	100.0	240	7	US-11-021-441-28
3	43	78.2	20	6	US-10-623-155-496
4	41	74.5	555	7	US-11-072-512-3369
5	41	74.5	953	7	US-11-037-243-66
6	40	72.7	678	7	US-11-072-512-3295
7	40	72.7	1832	7	US-11-087-099-7762
8	39	70.9	213	7	US-11-072-512-2722
9	39	70.9	233	7	US-11-240-769-58
10	39	70.9	430	6	US-10-992-577-8
11	39	70.9	430	6	US-10-508-892-2
12	39	70.9	430	7	US-11-223-294-54
13	39	70.9	618	7	US-11-078-735-18
14	39	70.9	618	7	US-11-050-346-63
15	39	70.9	618	7	US-11-103-077-18
16	39	70.9	662	7	US-11-072-175-184
17	38	69.1	128	7	US-11-096-568A-16457
18	38	69.1	236	7	US-11-096-568A-22845
19	38	69.1	274	7	US-11-096-568A-22803
20	38	69.1	306	7	US-11-096-568A-20556
21	38	69.1	320	7	US-11-096-568A-988
22	38	69.1	438	6	US-10-650-3268-9
23	38	69.1	459	7	US-11-096-568A-21887
24	37	67.3	134	7	US-11-096-568A-23806
25	37	67.3	189	7	US-11-107-029-4

26	37	67.3	198	7	US-11-096-568A-22494	Sequence 22494, A
27	37	67.3	269	7	US-11-096-568A-22493	Sequence 22493, A
28	37	67.3	379	7	US-11-109-156-16	Sequence 15, Appl
29	37	67.3	401	7	US-11-096-568A-382	Sequence 382, App
30	37	67.3	401	7	US-11-096-568A-383	Sequence 383, App
31	37	67.3	410	7	US-11-096-568A-381	Sequence 381, App
32	37	67.3	1465	7	US-11-087-099-1792	Sequence 1792, Ap
33	37	67.3	1465	7	US-11-087-099-10059	Sequence 10059, A
34	37	67.3	2923	7	US-11-200-822-3	Sequence 3, Appli
35	36.5	66.4	167	7	US-11-096-568A-10542	Sequence 10542, A
36	36.5	66.4	193	7	US-11-096-568A-21910	Sequence 21910, A
37	36.5	66.4	280	7	US-11-143-980-34	Sequence 34, Appl
38	36	65.5	55	7	US-11-114-325-14	Sequence 14, Appl
39	36	65.5	60	7	US-11-114-325-15	Sequence 15, Appl
40	36	65.5	107	7	US-11-145-861-3	Sequence 3, Appli
41	36	65.5	155	7	US-11-096-568A-19104	Sequence 19104, A
42	36	65.5	188	6	US-10-821-234-941	Sequence 941, App
43	36	65.5	237	7	US-11-096-568A-10553	Sequence 10553, A
44	36	65.5	238	7	US-11-194-890-12	Sequence 12, Appl
45	36	65.5	246	7	US-11-087-099-6549	Sequence 6549, Ap

ALIGNMENTS

RESULT 1

US-11-155-288-7
; Sequence 7, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J. L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANKK.050A
; CURRENT APPLICATION NUMBER: US/11/155,288
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-7

Query Match 100.0%; Score 55; DB 7; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASGPGGGAPR 10
DB 53 ASGPGGGAPR 62

RESULT 2

US-11-021-441-28
; Sequence 28, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LOCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06

; PRIOR APPLICATION NUMBER: US 60/615,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein
US-11-021-441-28

Query Match 100.0%; Score 55; DB 7; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGAPR 10
|||||
DB 113 ASGPGGGAPR 122

RESULT 3

US-10-623-155-496
; Sequence 496, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 496
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-496

Query Match 78.2%; Score 43; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASGPGGGA 8
|||||
DB 13 ASGPGGGA 20

RESULT 4

US-11-072-512-3369
; Sequence 3369, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:

; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO

; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3369
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3369

Query Match 74.5%; Score 41; DB 7; Length 555;
Best Local Similarity 77.8%; Pred. No. 76;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASGPGGGAP 9
|||||
DB 473 ASGPGGGSP 481

RESULT 5

US-11-037-243-66
; Sequence 66, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:

; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARIDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 953
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-66

Query Match 74.5%; Score 41; DB 7; Length 953;
Best Local Similarity 87.5%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGGGAPR 10
|||||
DB 214 GPGGGHR 221

RESULT 6

US-11-072-512-3295

Sequence 3295, Application US/11072512
 Publication No. US20060029945A1
 GENERAL INFORMATION:
 APPLICANT: ISOGAI, TAKAO
 APPLICANT: SUGIYAMA, TOMOYASU
 APPLICANT: OTSUKI, TETSUJI
 APPLICANT: WAKAMATSU, AI
 APPLICANT: SATO, HIROYUKI
 APPLICANT: ISHII, SHIZUKO
 APPLICANT: YAMAMOTO, JUN-ICHI
 APPLICANT: ISONO, YUUKO
 APPLICANT: HIO, YURI
 APPLICANT: OTSUKA, KAORU
 APPLICANT: NAGAI, KEIICHI
 APPLICANT: IRIE, RYOTARO
 APPLICANT: TAMECHIKA, ICHIRO
 APPLICANT: SEKI, NAOHICO
 APPLICANT: YOSHIKAWA, TSUTOMU
 APPLICANT: OTSUKA, MOTYUKI
 APPLICANT: NAGAHARI, KENJI
 APPLICANT: MASUHO, YASUHIKO
 TITLE OF INVENTION: Novel full length cDNA
 FILE REFERENCE: 084335-0191
 CURRENT APPLICATION NUMBER: US/11/072,512
 CURRENT FILING DATE: 2005-03-07
 PRIOR APPLICATION NUMBER: US 60/350,978
 PRIOR FILING DATE: 2002-01-25
 PRIOR APPLICATION NUMBER: JP 2001-379298
 PRIOR FILING DATE: 2001-11-05
 NUMBER OF SEQ ID NOS: 4096
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3295
 LENGTH: 678
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-072-512-3295

Query Match 72.7%; Score 40; DB 7; Length 678;
 Best Local Similarity 77.8%; Pred. No. 1.2e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASGPGGGAP 9
 | : | | | | |
 Db 593 AAGPGGGGP 601

RESULT 7
 US-11-087-099-7762
 Sequence 7762, Application US/11087099
 Publication No. US20060041961A1
 GENERAL INFORMATION:
 APPLICANT: Abad, Mark S. et al.
 TITLE OF INVENTION: Genes and Uses for Plant Improvement
 FILE REFERENCE: 38-21(53450)B EP
 CURRENT APPLICATION NUMBER: US/11/087,099
 CURRENT FILING DATE: 2005-03-22
 NUMBER OF SEQ ID NOS: 12464
 SEQ ID NO 7762
 LENGTH: 1832
 TYPE: PRT
 ORGANISM: Podospora anserina
 US-11-087-099-7762

Query Match 72.7%; Score 40; DB 7; Length 1832;
 Best Local Similarity 77.8%; Pred. No. 2.8e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SGPGGGAPR 10
 | | | | | | |
 Db 1051 SGSGGGSPR 1059

RESULT 8

US-11-072-512-2722
 Sequence 2722, Application US/11072512
 Publication No. US20060029945A1
 GENERAL INFORMATION:
 APPLICANT: ISOGAI, TAKAO
 APPLICANT: SUGIYAMA, TOMOYASU
 APPLICANT: OTSUKI, TETSUJI
 APPLICANT: WAKAMATSU, AI
 APPLICANT: SATO, HIROYUKI
 APPLICANT: ISHII, SHIZUKO
 APPLICANT: YAMAMOTO, JUN-ICHI
 APPLICANT: ISONO, YUUKO
 APPLICANT: HIO, YURI
 APPLICANT: OTSUKA, KAORU
 APPLICANT: NAGAI, KEIICHI
 APPLICANT: IRIE, RYOTARO
 APPLICANT: TAMECHIKA, ICHIRO
 APPLICANT: SEKI, NAOHICO
 APPLICANT: YOSHIKAWA, TSUTOMU
 APPLICANT: OTSUKA, MOTYUKI
 APPLICANT: NAGAHARI, KENJI
 APPLICANT: MASUHO, YASUHIKO
 TITLE OF INVENTION: Novel full length cDNA
 FILE REFERENCE: 084335-0191
 CURRENT APPLICATION NUMBER: US/11/072,512
 CURRENT FILING DATE: 2005-03-07
 PRIOR APPLICATION NUMBER: US 60/350,978
 PRIOR FILING DATE: 2002-01-25
 PRIOR APPLICATION NUMBER: JP 2001-379298
 PRIOR FILING DATE: 2001-11-05
 NUMBER OF SEQ ID NOS: 4096
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2722
 LENGTH: 213
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-072-512-2722

Query Match 70.9%; Score 39; DB 7; Length 213;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SGPGGGA 8
 | | | | | | |
 Db 56 SGPGGGA 62

RESULT 9
 US-11-240-769-58
 Sequence 58, Application US/11240769
 Publication No. US20060036089A1
 GENERAL INFORMATION:
 APPLICANT: Soppet et al.
 TITLE OF INVENTION: 33 Human Secreted Proteins
 FILE REFERENCE: P2037P1C2
 CURRENT APPLICATION NUMBER: US/11/240,769
 CURRENT FILING DATE: 2003-10-03
 PRIOR APPLICATION NUMBER: 09/997,131
 PRIOR FILING DATE: 2001-11-30
 PRIOR APPLICATION NUMBER: 09/628,508
 PRIOR FILING DATE: 2000-07-28
 PRIOR APPLICATION NUMBER: PCT/US00/03062
 PRIOR FILING DATE: 2000-02-08
 PRIOR APPLICATION NUMBER: 60/119,468
 PRIOR FILING DATE: 1999-02-10
 NUMBER OF SEQ ID NOS: 173
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 58
 LENGTH: 233
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE

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; LOCATION: (168)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-11-240-769-58

Query Match          70.9%; Score 39; DB 7; Length 233;
Best Local Similarity 87.5%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGGGGAPR 10
   ||| |||
Db 40 GPGGGAPR 47

RESULT 10
US-10-992-577-8
; Sequence 8, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 57155-D/JPW
; CURRENT APPLICATION NUMBER: US/10/992,577
; CURRENT FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-992-577-8

Query Match          70.9%; Score 39; DB 6; Length 430;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 SGPGGGAPR 10
   ||| |||
Db 387 SGPGSGAPR 395

RESULT 11
US-10-508-892-2
; Sequence 2, Application US/10508892
; Publication No. US20060014218A1
; GENERAL INFORMATION:
; APPLICANT: Golz, Stefan
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Weingartner, Bernhard
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
; TITLE OF INVENTION: Neuropeptide FF Receptor 1 (NPFF1)
; FILE REFERENCE: Le A 35 944
; CURRENT APPLICATION NUMBER: US/10/508,892
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: PCT/EP03/02685
; PRIOR FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: EP 02006654.4
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2

Query Match          70.9%; Score 39; DB 7; Length 430;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 SGPGGGAPR 10
   ||| |||
Db 387 SGPGSGAPR 395

RESULT 12
US-11-223-294-54
; Sequence 54, Application US/11223294
; Publication No. US2006003532A1
; GENERAL INFORMATION:
; APPLICANT: HINUMA, Shuji
; APPLICANT: YOSHIDA, Hiromi
; APPLICANT: HABATA, Yugo
; APPLICANT: HOSOYA, Masaki
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: Novel RFRP-3 And Its DNA
; FILE REFERENCE: 2944USOP
; CURRENT APPLICATION NUMBER: US/11/223,294
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: US/10/487,634
; PRIOR FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: PCT/JP02/08466
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: JP 2001-254826
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 54
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Human
US-11-223-294-54

Query Match          70.9%; Score 39; DB 7; Length 430;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 SGPGGGAPR 10
   ||| |||
Db 387 SGPGSGAPR 395

RESULT 13
US-11-078-735-18
; Sequence 18, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAM JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
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;; PRIOR FILING DATE: 2002-11-13
;; PRIOR APPLICATION NUMBER: PCT/GB02/05133
;; PRIOR FILING DATE: 2002-11-13
;; PRIOR APPLICATION NUMBER: GB 0220912.0
;; PRIOR FILING DATE: 2002-09-10
;; PRIOR APPLICATION NUMBER: GB 0220913.8
;; PRIOR FILING DATE: 2002-09-10
;; NUMBER OF SEQ ID NOS: 51
;; SOFTWARE: PatentIn Ver. 3.3
;; SEQ ID NO 18
;; LENGTH: 618
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-078-735-18

Query Match 70.9%; Score 39; DB 7; Length 618;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GPGGAPR 10
||| ||||
Db 40 GPGGAPR 47

RESULT 14
US-11-050-346-63
;; Sequence 63, Application US/11050346
;; Publication No. US2006002924A1
;; GENERAL INFORMATION:
;; APPLICANT: BODMER, MARK WILLIAM
;; APPLICANT: CHAMPION, BRIAN ROBERT
;; APPLICANT: LENNARD, ANDREW CHRISTOPHER
;; APPLICANT: MCKENZIE, GRAHAME JAMES
;; APPLICANT: TUGAL, TAMARA
;; APPLICANT: WARD, GEORGE ALBERT
;; TITLE OF INVENTION: CONJUGATE OF NOTCH SIGNALLING PATHWAY MODULATORS AND
;; FILE REFERENCE: 674525-2016
;; CURRENT APPLICATION NUMBER: US/11/050,346
;; CURRENT FILING DATE: 2005-02-03
;; PRIOR FILING DATE: 2003-05-24
;; PRIOR APPLICATION NUMBER: PCT/GB03/01525
;; PRIOR FILING DATE: 2003-04-04
;; PRIOR APPLICATION NUMBER: GB 0300234.2
;; PRIOR FILING DATE: 2003-01-07
;; PRIOR APPLICATION NUMBER: GB 0218068.5
;; PRIOR FILING DATE: 2002-08-03
;; PRIOR APPLICATION NUMBER: GB 0220849.4
;; PRIOR FILING DATE: 2002-09-07
;; PRIOR APPLICATION NUMBER: GB 0220912.0
;; PRIOR FILING DATE: 2002-09-10
;; PRIOR APPLICATION NUMBER: GB 0220913.8
;; PRIOR FILING DATE: 2002-09-10
;; PRIOR APPLICATION NUMBER: PCT/GB02/05137
;; PRIOR FILING DATE: 2002-11-13
;; PRIOR APPLICATION NUMBER: PCT/GB02/05133
;; PRIOR FILING DATE: 2002-11-13
;; NUMBER OF SEQ ID NOS: 69
;; SOFTWARE: PatentIn Ver. 3.3
;; SEQ ID NO 63
;; LENGTH: 618
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-050-346-63

Query Match 70.9%; Score 39; DB 7; Length 618;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GPGGAPR 10
||| ||||
Db 40 GPGGAPR 47

RESULT 15
US-11-103-077-18
;; Sequence 18, Application US/11103077
;; Publication No. US20060003927A1
;; GENERAL INFORMATION:
;; APPLICANT: CHAMPION, BRIAN ROBERT
;; APPLICANT: YOUNG, LESLEY LYNN
;; TITLE OF INVENTION: MODULATION OF IMMUNE FUNCTION
;; FILE REFERENCE: 674525-2020
;; CURRENT APPLICATION NUMBER: US/11/103,077
;; CURRENT FILING DATE: 2005-04-11
;; PRIOR APPLICATION NUMBER: PCT/GB03/04402
;; PRIOR FILING DATE: 2003-10-09
;; PRIOR APPLICATION NUMBER: GB 0223405.2
;; PRIOR FILING DATE: 2002-10-09
;; PRIOR APPLICATION NUMBER: GB 0223409.4
;; PRIOR FILING DATE: 2002-10-09
;; PRIOR APPLICATION NUMBER: GB 0224353.3
;; PRIOR FILING DATE: 2002-10-19
;; NUMBER OF SEQ ID NOS: 29
;; SOFTWARE: PatentIn Ver. 3.3
;; SEQ ID NO 18
;; LENGTH: 618
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-103-077-18

Query Match 70.9%; Score 39; DB 7; Length 618;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GPGGAPR 10
||| ||||
Db 40 GPGGAPR 47

Search completed: March 13, 2006, 20:03:30
Job time : 7.82353 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 18:52:59 ; Search time 112.941 Seconds
(without alignments)
59.355 Million cell updates/sec

Title: US-09-529-206E-26

Perfect score: 78

Sequence: 1 AGAARASGPGGAPR 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	15	2	AAY05978 Human can
2	78	100.0	20	2	AAY05979 Human can
3	78	100.0	30	5	Aau85105 Human NYN
4	78	100.0	179	8	Adk68648 Epitope 1
5	78	100.0	180	2	Aaw62584 Cancer as
6	78	100.0	180	2	Aaw65965 Human NY-
7	78	100.0	180	2	AAY05965 Human can
8	78	100.0	180	3	AAY52430 Human tum
9	78	100.0	180	3	AAY70862 Human tum
10	78	100.0	180	3	AAB03154 Human oes
11	78	100.0	180	4	AAB69946 Human NY-
12	78	100.0	180	4	AAG67164 Amino aci
13	78	100.0	180	4	Aau01535 Human NY-
14	78	100.0	180	4	Aae07714 Human NY-
15	78	100.0	180	5	Aau84818 Human NYN
16	78	100.0	180	5	Aau11543 Human tum
17	78	100.0	180	6	ABR58672 Human can
18	78	100.0	180	6	ABR48210 Human bla
19	78	100.0	180	6	ABU56508 Lung canc
20	78	100.0	180	6	ABU56694 Lung canc
21	78	100.0	180	6	ABP74198 Human NY-
22	78	100.0	180	6	ABU64816 Human NY-
23	78	100.0	180	6	ABR83438 Human NY-
24	78	100.0	180	7	ADC09576 NY-ESO-1

25	78	100.0	180	7	ADD35564	Add35564 Human NY-
26	78	100.0	180	7	ADD35568	Add35568 Human NY-
27	78	100.0	180	7	ADD25510	Add25510 Binding d
28	78	100.0	180	7	ADN39068	Adn39068 Cancer/an
29	78	100.0	180	8	ADJ54139	Adj54139 Human NY-
30	78	100.0	180	8	ADM72815	Adm72815 Human NY-
31	78	100.0	180	8	ADM73418	Adm73418 CAG-3 pro
32	78	100.0	180	8	ADM73417	Adm73417 Human NY-
33	78	100.0	180	8	ADQ18451	Adq18451 Human sof
34	78	100.0	180	8	ADQ10446	Adq10446 Autolmmun
35	78	100.0	180	8	ADS80926	Ads80926 Tumour as
36	78	100.0	180	9	ADW44353	Adw44353 Human aut
37	78	100.0	180	9	ADY85096	Ady85096 Tumor ant
38	78	100.0	180	9	ADZ28913	Adz28913 NY-ESO-1
39	78	100.0	180	9	ADZ42374	Adz42374 Immunogen
40	78	100.0	180	9	AEA35651	Aea35651 Human NY-
41	78	100.0	240	9	AEW99402	Aew99402 NY-ESO-1/
42	78	100.0	240	9	AE880047	Aeb80047 Human NY-
43	78	100.0	397	4	AAE13122	Aae13122 NY-ESO-1C
44	78	100.0	3541	5	AAU95130	Aau95130 Human mel
45	74	94.9	14	2	AAY05986	Aay05986 Human can

ALIGNMENTS

RESULT 1

AAY05978

ID AAY05978 standard; peptide; 15 AA.

XX

AC AAY05978;

XX

DT 16-AUG-1999 (first entry)

XX

DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.

XX

KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine.

XX Homo sapiens.

OS

XX

PN WO9918206-A2.

XX

PD 15-APR-1999.

XX

PF 21-SEP-1998; 98WO-US019609.

XX

PR 08-OCT-1997; 97US-0061428P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Wang RF, Rosenberg SA;

XX

DR WPI; 1999-277270/23.

XX

PT Cancer antigen NY ESO1/CAG-3.

XX

PS Claim 15; Page 64; 88pp; English.

XX

CC The present sequence represents a cancer peptide that corresponds to
 CC amino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
 CC AAY05965), a new and potent tumour antigen capable of eliciting an
 CC antigen specific immune response by T cells. Cancer peptides derived from
 CC CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
 CC variants (see AAY05967-87), are useful as cancer vaccines that protect
 CC against cancer. The invention provides: vectors and host cells (also
 CC useful as vaccines); a method of diagnosis of cancer or precancer; a
 CC transgenic animal; antisense oligonucleotides that inhibit expression of

CC the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
 CC cancer peptide, useful in diagnostic and detection assays; and methods
 CC for preventing or inhibiting cancer by administering a cancer peptide,
 CC with or without an HLA molecule. The cancer peptides form part of, or are
 CC derived from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
 CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
 CC treated by inducing cancer-specific T cells in vitro for subsequent
 CC return to a patient
 XX
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 78; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAPR 15
 |||||
 DB 1 AGAARASGPGGAPR 15

RESULT 2
 AAY05979
 ID AAY05979 standard; peptide; 20 AA.
 XX
 AC AAY05979;

DT 16-AUG-1999 (first entry)
 XX Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine.

XX Homo sapiens.
 OS Synthetic.

XX WO9918206-A2.

XX 15-APR-1999.

XX 21-SEP-1998; 98WO-US019609.

XX 08-OCT-1997; 97US-0061428P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang RF, Rosenberg SA;

XX WPI; 1999-277270/23.

XX Cancer antigen NY ESO1/CAG-3.

XX Claim 16; Page 64; 88pp; English.

XX The present sequence represents a cancer peptide that is based on amino
 CC acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965),
 CC a new and potent tumour antigen capable of eliciting an antigen specific
 CC immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-
 CC 3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-
 CC 87), are useful as cancer vaccines that protect against cancer. The
 CC invention provides vectors and host cells (also useful as vaccines); a
 CC method of diagnosis of cancer or precancer; a transgenic animal;
 CC antisense oligonucleotides that inhibit expression of the cancer peptide
 CC or tumour antigen; antibodies reacting with a CAG-3 cancer peptide,
 CC useful in diagnostic and detection assays; and methods for preventing or
 CC inhibiting cancer by administering a cancer peptide, with or without an

CC HLA molecule. The cancer peptides form part of, or are derived from,
 CC cancers such as primary or metastatic melanoma, thymoma, lymphoma,
 CC sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
 CC cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
 CC prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by
 CC inducing cancer-specific T cells in vitro for subsequent return to a
 CC patient
 XX
 XX
 SQ Sequence 20 AA;

Query Match 100.0%; Score 78; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.0037;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAPR 15
 |||||
 DB 6 AGAARASGPGGAPR 20

RESULT 3
 AAU85105
 ID AAU85105 standard; peptide; 30 AA.
 XX
 AC AAU85105;

DT 08-MAY-2002 (first entry)

XX Human NYNSola segment 4.

XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
 KW viral infection; human immunodeficiency virus; melanoma;
 KW bacterial infection; Salmonella; Legionella; parasitic infection;
 KW Trypanosoma; Toxoplasma; Giardia.

XX Homo sapiens.

XX WO200190197-A1.

XX 29-NOV-2001.

XX 25-MAY-2001; 2001WO-AU000622.

XX 26-MAY-2000; 2000AU-00007761.

XX (AUSU) UNIV AUSTRALIAN NAT.

XX Thomson SA, Ramshaw IA;

XX WPI; 2002-147575/19.

XX N-PSDB; ABK36925.

XX New synthetic polypeptides having several different segments of at least
 PT one parent polypeptide linked together differently compared to the
 PT linkage in the parent polypeptide, for inducing immune response against a
 PT pathogen or cancer.

XX Example 3; Fig 27; 364pp; English.

XX The invention relates to a new synthetic polypeptide (I) comprising
 CC several different segments of at least one parent polypeptide linked
 CC together in a different relationship relative to their linkage in the
 CC parent polypeptide to impede, abrogate or otherwise alter at least one
 CC function associated with the parent polypeptide and for inducing an
 CC immune response against a pathogen or cancer. Also included are a
 CC synthetic polynucleotide encoding and a computer system for designing the
 CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
 CC are referred to as a Savine. The synthetic polypeptide is useful for
 CC modulating immune responses preferably directed against a pathogen or a
 CC cancer. (e.g., cancers of the lung, breast, ovary, cervix, colon, head
 CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
 CC oesophagus, brain, testicle, uterus), as potentiating agents.
 CC Compositions comprising the polypeptide may be used in the treatment or
 CC prophylaxis against viral (such as infections caused by HIV (human

CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
 CC (e.g., infections caused by Neisseria, Meningococcus, Haemophilus,
 CC Salmonella, Streptococcus, Legionella and Mycobacterium or parasitic
 CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
 CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
 CC a peptide derived from a parent protein used to construct a vaccine of the
 CC invention

XX Sequence 30 AA;

Query Match 100.0%; Score 78; DB 5; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0054;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAPR 15
 DB 5 AGAARASGPGGAPR 19
 |||||

RESULT 4
 ADK68648
 ID ADK68648 standard; protein; 179 AA.

XX AC ADK68648;

XX DT 06-MAY-2004 (first entry)

XX DE Epitope liberation-related NY-ESO-1 protein SeqID11.

XX KW epitope liberation; substrate; proteasome; cytostatic; antibacterial;
 KW protozoasidic; fungicide; T-cell activator; vaccine; housekeeping epitope;
 KW cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;
 KW virus; bacterium; protozoan; fungus; housekeeping proteasome system;
 KW human.

XX OS Homo sapiens.

XX PN US2003228634-A1.

XX PD 11-DEC-2003.

XX PF 07-NOV-2002; 2002US-00292413.

XX PR 07-NOV-2001; 2001US-0336968P.

XX PA (SIMA/) SIMARD J J L.

XX PA (DIAM/) DIAMOND D C.

XX PA (QIUZ/) QIU Z.

XX PA (LEIX/) LEI X.

XX PI Simard J J L, Diamond DC, Qiu Z, Lei X;

XX DR WPI; 2004-167209/16.

XX DR N-PSDB; ADK68674.

XX FT Identifying polypeptide suitable for epitope e.g., housekeeping epitope,
 FT liberation by contacting substrate polypeptide comprising epitope of
 FT interest, with proteasome, and assaying for liberation of epitope.

XX PS Example 2; SEQ ID NO 11; 67pp; English.

XX CC This invention relates to a novel method of identifying a polypeptide
 CC suitable for epitope liberation, including the steps of identifying an
 CC epitope of interest; providing substrate polypeptide sequence including
 CC the epitope, wherein the substrate permits processing by a proteasome;
 CC contacting the substrate with a composition including the proteasome,
 CC under conditions that support processing of the substrate by proteasome;
 CC and assaying for liberation of epitope. The invention may be useful for
 CC the development of compounds with a cytostatic, antibacterial,
 CC protozoasidic or fungicidal activity acting as T-cell activators. In
 CC addition, the invention may allow development of a vaccine. The invention
 CC is useful for identifying a polypeptide suitable for epitope liberation,

CC where the epitope is a housekeeping epitope. The compositions comprising
 CC the identified housekeeping epitopes are useful in vitro in vaccine
 CC development or in the generation or expansion of cytotoxic T lymphocyte
 CC (CTL) to be used in adoptive immunotherapy. The invention is also useful
 CC for activating T-cells against neoplastic cells, and cells infected with
 CC virus, bacterium, protozoan or fungus. CTL epitopes are identified based
 CC on the knowledge that such epitopes are, in fact, produced by the
 CC housekeeping proteasome system. Once identified, these epitopes, embodied
 CC as peptides, can be used to successfully immunise or induce therapeutic
 CC CTL responses against housekeeping proteasome expressing target cells in
 CC the host. The present sequence is that of a protein which is related to
 CC the method of the invention.

XX SQ Sequence 179 AA;

Query Match 100.0%; Score 78; DB 8; Length 179;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAPR 15
 DB 47 AGAARASGPGGAPR 61
 |||||

RESULT 5

AAW62584

ID AAW62584 standard; protein; 180 AA.

XX AC AAW62584;

XX DT 17-SEP-1998 (first entry)

XX DE Cancer associated antigen NY-ESO-1.

XX KW Cancer associated antigen; NY-ESO-1; regression; progression; onset;
 KW cancer; treatment; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 7 /note= "potential myristoylation site"

FT Misc-difference 9 /note= "potential myristoylation site"

FT Misc-difference 11 /note= "potential phosphorylation site"

FT Misc-difference 98 /note= "potential phosphorylation site"

FT Misc-difference 134 /note= "potential phosphorylation site"

FT Misc-difference 138 /note= "potential phosphorylation site"

FT Misc-difference 138 /note= "potential phosphorylation site"

XX PN WO9814464-A1.

XX PD 09-APR-1998.

XX PF 15-SEP-1997; 97WO-US016335.

XX PR 03-OCT-1996; 96US-00725182.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Chen Y, Scanlan M, Gure A, Old LJ, Jager E, Knuth A;

XX PI Drijfhout JW;

XX DR WPI; 1998-286417/25.

XX DR N-PSDB; AAV38566.

XX CC New isolated cancer associated antigen - is used to develop products for
 PT the diagnosis and treatment of cancers and for monitoring cancer therapy.
 XX Claim 8; Fig 3; 49pp; English.

XX The present sequence represents a cancer associated antigen. The clone
 CC from which the DNA sequence is obtained is designated NY-ESO-1. The
 CC specification described a method for determining regression, progression
 CC of onset of a cancerous condition, comprising monitoring a sample from a
 CC patient with the cancerous condition for a parameter selected from NY-ESO
 CC -1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells
 CC specific for the peptide and an MHC molecule with which it non-covalently
 CC complexes. Methods for the treatment of a cancerous condition are also
 CC described. The NY-ESO-1 protein and peptides derived from it can be used
 CC for diagnosis and treatment of cancers and to monitor the efficacy of a
 CC therapeutic regime
 CC
 XX Sequence 180 AA;
 SQ
 Query Match 100.0%; Score 78; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGAARASGPGGAPR 15
 Db |||||
 48 AGAARASGPGGAPR 62
 RESULT 6
 AAW69665
 ID AAW69665 standard; protein; 180 AA.
 XX
 AC AAW69665;
 XX
 DT 27-OCT-1998 (first entry)
 XX
 DE Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
 XX
 KW Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO9832855-A1.
 XX
 PD 30-JUL-1998.
 XX
 PF 27-JAN-1998; 98WO-US001445.
 XX
 PR 27-JAN-1997; 97US-00791495.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Lethe B, Lucas S, De Smet C, Godelaine D, Boon-Falleur T;
 XX
 DR WPI; 1998-427951/36.
 DR N-PSDB; AAV50348.
 XX
 PT New isolated LAGE-1 tumour associated nucleic acids - used to develop
 PT products for the diagnosis and treatment of LAGE-1 associated disorders,
 PT particularly tumours.
 XX
 XX Example 2; Page 57-58; 73pp; English.
 PS
 SS The present sequence represents human NY-ESO-1, formerly known as LL-1.2
 CC clone, which is used in an example from the present invention which
 CC describes LAGE-1 tumour associated protein (TAP). The present invention
 CC also describes: (1) a method for treating a subject with a disorder
 CC characterised by expression of a LAGE-1 nucleic acid molecule or an
 CC expression product, comprising administering to the subject autologous
 CC cytolytic T cells to ameliorate the disorder, where the cytolytic T cells
 CC are specific for complexes of an HLA molecule and a LAGE-1 TAP or an
 CC immunogenic fragment; (2) a method for treating a subject with a disorder
 CC characterised by expression of a LAGE-1 nucleic acid molecule or an
 CC expression product, comprising administering a LAGE-1 TAP or an
 CC immunogenic fragment to ameliorate the disorder; and (3) a method for
 CC selectively enriching a population of T cells with cytolytic T cells
 CC specific for a LAGE-1 TAP comprising contacting an isolated population of

CC T cells with an agent presenting a complex of a LAGE TAP or an
 CC immunogenic fragment and a HLA presenting molecule to selectively enrich
 CC the isolated population of T cells with the cytolytic T cells. The
 CC methods and products from the present invention can be used for the
 CC diagnosis and treatment of LAGE-1 associated disorders, particularly
 CC tumours
 XX
 SQ Sequence 180 AA;
 Query Match 100.0%; Score 78; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGAARASGPGGAPR 15
 Db |||||
 48 AGAARASGPGGAPR 62
 RESULT 7
 AAY05965
 ID AAY05965 standard; protein; 180 AA.
 XX
 AC AAY05965;
 XX
 DT 16-AUG-1999 (first entry)
 XX
 DE Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.
 XX
 KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia;
 KW non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis;
 KW melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer;
 KW breast cancer; prostate cancer; ovarian cancer; cervical cancer;
 KW bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma;
 KW tumour; diagnosis; immunotherapy; therapy; vaccine; ORF1.
 XX
 OS Homo sapiens.
 XX
 PN WO9918206-A2.
 XX
 PD 15-APR-1999.
 XX
 PF 21-SEP-1998; 98WO-US019609.
 XX
 PR 08-OCT-1997; 97US-0061428P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Wang RF, Rosenberg SA;
 XX
 DR WPI; 1999-277270/23.
 DR N-PSDB; AAX58599.
 XX
 PT Cancer antigen NY ESO1/CAG-3.
 XX
 PS Claim 4; Fig 3A; 88pp; English.
 XX
 CC The present sequence represents the ORF1 protein encoded by open reading
 CC frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and
 CC potent tumour antigen capable of eliciting an antigen specific immune
 CC response by T cells. Cancer peptides comprising ORF1, ORF2 (see
 CC AAY05966), portions of these peptides and their variants (see AAY05965-
 CC 87), are useful as cancer vaccines that protect the recipient from
 CC development of cancer. The invention provides: vectors and host cells
 CC (also useful as vaccines); a method of diagnosis of cancer or precancer;
 CC a transgenic animal; antisense oligonucleotides that inhibit expression
 CC of the cancer peptide or tumour antigen; antibodies reacting with the CAG
 CC -3 cancer peptide, useful in diagnostic and detection assays; and methods
 CC for preventing or inhibiting cancer by administering a cancer peptide,
 CC with or without an HLA molecule. The cancer peptides form part of, or are
 CC derived from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
 CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is

CC treated by inducing cancer-specific T cells in vitro for subsequent
 CC return to a patient
 XX
 SQ Sequence 180 AA;

Query Match 100.0%; Score 78; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. NO. 0.027;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARAAGPGGAPR 15
 |||||
 Db 48 AGAARAAGPGGAPR 62

RESULT 8
 AAY52430
 ID AAY52430 standard; protein; 180 AA.

XX AC AAY52430;

XX DT 21-OCT-2004 (revised)

XX DT 15-FEB-2000 (first entry)

XX DE Human tumour antigen NY-ESO-1.

KW Cancer; tumour; antigen; MHC; major histocompatibility complex; T-cell;
 KW cytotoxic; helper; stimulation; proliferation; treatment; diagnosis;
 KW prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;
 KW hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.

XX OS Homo sapiens.

XX OS Unidentified.

FH Key Location/Qualifiers
 FT Peptide 44..53

FT /note= "Peptide presented by MHC Class I HLA-B7"

FT Peptide 60..69

FT /note= "Peptide presented by MHC Class I HLA-B7"

FT Peptide 60..68

FT /note= "Peptide presented by MHC Class I HLA-B7"

FT Peptide 63..72

FT /note= "Peptide presented by MHC Class I HLA-B7"

FT Peptide 79..88

FT /note= "Peptide presented by MHC Class I HLA-B7"

FT Peptide 79..87

FT /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
 and HLA-B35"

FT Peptide 82..91

FT /note= "Peptide presented by MHC Class I HLA-A1"

FT Peptide 82..90

FT /note= "Peptide presented by MHC Class I HLA-A1"

FT Peptide 83..91

FT /note= "Peptide presented by MHC Class I HLA-B44"

FT Peptide 84..92

FT /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
 and HLA-B35"

FT Peptide 87..96

FT /note= "Peptide presented by MHC Class I HLA-A1"

FT Peptide 88..96

FT /note= "Peptide presented by MHC Class I HLA-B44"

FT Peptide 96..104

FT /note= "Peptide presented by MHC Class I HLA-B7"

FT Peptide 100..108

FT /note= "Peptide presented by MHC Class I HLA-B44"

FT Peptide 102..110

FT /note= "Peptide presented by MHC Class I HLA-B44"

FT Peptide 107..116

FT /note= "Peptide presented by MHC Class I HLA-A24"

FT Peptide 110..118

FT /note= "Peptide presented by MHC Class I HLA-B52"

FT Peptide 113..122

FT /note= "Peptide presented by MHC Class I HLA-B7 and HLA-
 B52"

FT Peptide 113..121
 FT /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 115..124
 FT /note= "Peptide presented by MHC Class I HLA-A3"
 FT Peptide 118..126
 FT /note= "Peptide presented by MHC Class I HLA-B35"
 FT Peptide 124..133
 FT /note= "Peptide presented by MHC Class I HLA-B52"
 FT Peptide 125..133
 FT /note= "Peptide presented by MHC Class I HLA-A24"
 FT Peptide 138..147
 FT /note= "Peptide presented by MHC Class I HLA-B8"
 FT Peptide 139..147
 FT /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 145..153
 FT /note= "Peptide presented by MHC Class I HLA-A24 and HLA-
 B52"
 FT Peptide 153..162
 FT /note= "Peptide presented by MHC Class I HLA-B52"
 FT Peptide 154..163
 FT /note= "Peptide presented by MHC Class I HLA-B52"
 FT Peptide 154..162
 FT /note= "Peptide presented by MHC Class I HLA-B52"
 FT Peptide 156..167
 FT /note= "Peptide (AAY52434) presented by MHC Class I HLA-
 A2"
 FT Peptide 158..166
 FT /note= "Peptide presented by MHC Class I HLA-A3"
 FT Peptide 159..167
 FT /note= "Peptide presented by MHC Class I HLA-A3"
 FT Peptide 162..170
 FT /note= "Peptide presented by MHC Class I HLA-B52"

XX W0953938-A1.

XX 28-OCT-1999.

XX 24-MAR-1999; 99WO-US006875.

XX 17-APR-1998; 98US-00062422.

XX 02-OCT-1998; 98US-00165546.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;

XX Gure A, Ritter G;

XX WPI; 2000-038483/03.

XX N-PSDB; AA238380.

XX Novel peptides which bind to MHC class I and MHC class II molecules,
 useful for therapeutic and diagnostic purposes.

XX Claim 30; Fig 3; 49pp; English.

XX This sequence represents a human tumour antigen, NY-ESO-1, the cDNA
 encoding which was isolated from an oesophagus squamous cell cancer cDNA
 library. Tissue localisation studies revealed it to be expressed at high
 levels in normal ovary and testis but not in normal colon, kidney, liver,
 brain, oesophagus and skin. It was expressed in certain tumours and
 tumour cell lines with some degree of frequency - these included melanoma
 specimens and cell lines, and breast and bladder cancer specimens, with
 expression in other tumour types being sporadic. Peptides derived from NY
 -ESO-1 are bound by both MHC (major histocompatibility complex) Class I
 and Class II molecules for presentation to T-cells. Peptides AAY52431-
 Y52434 bind to Class I HLA-A2 molecules, thereby stimulating
 proliferation of cytotoxic T-cells, while peptides AAY52435-Y52440 bind
 to Class II HLA-DR53 molecules, stimulating helper T-cell proliferation.
 The peptides derived from NY-ESO-1 may be used in methods and
 compositions used for the treatment, diagnosis and prevention of cancers
 (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma,
 ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to
 stimulate the proliferation of T cells

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CC CC Revised record issued on 21-OCT-2004 : Correction to feature table key
XX SQ Sequence 180 AA;
    Query Match      100.0%; Score 78; DB 3; Length 180;
    Best Local Similarity 100.0%; Pred. No. 0.027;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAPR 15
    |||||
Db 48 AGAARASGPGGAPR 62

RESULT 9
AAY70862
ID AAY70862 standard; protein; 180 AA.
XX AC AAY70862;
XX DT 31-JUL-2000 (first entry)
XX DE Human tumour antigen, NY-ESO-1 protein.
XX KW NY-ESO-1; CAMEL; CTL-recognised Antigen on MELANOMA; human; cancer; CTL;
XX cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer;
XX melanoma; immunotherapy; immune response.
XX OS Homo sapiens.
XX PN WO200023584-A1.
XX PD 27-APR-2000.
XX PF 15-OCT-1999; 99WO-EP007832.
XX PR 16-OCT-1998; 98EP-00119583.
XX PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX PA (UYHO-) UNIV HOSPITAL LEIDEN.
XX PI Schrier PI, Aarnoudse CA, Heider K, Klade C;
XX WPI; 2000-339685/29.
XX DR N-PSDB; AAD00152.
XX PT Tumor-associated antigen useful for cancer immunotherapy is encoded by
XX the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
XX PS Example 3; Page 62-63; 73pp; English.
XX CC The present sequence is the human NY-ESO-1 protein, a tumour antigen,
XX identified by screening an esophagus carcinoma cDNA library. This protein
XX is derived from open reading frame (ORF)-1 that contain epitopes of
XX tumour specific T-cells. NY-ESO-1 is expressed in different tumour types,
XX but not in healthy tissues except in testis. It also shows homology with
XX the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELANOMA)
XX protein, a tumour-associated antigen. The tumour-associated antigen
XX displayed on melanoma cells is recognised by cytotoxic T lymphocytes.
XX This sequence has anticancer activity. CAMEL tumour antigen and
XX immunogenic peptides derived from it are useful for cancer immunotherapy.
XX They have the potential to induce an immune response, by eliciting a CTL
XX response. The DNA molecule is used for the construction of recombinant or
XX fusion proteins
XX SQ Sequence 180 AA;
    Query Match      100.0%; Score 78; DB 3; Length 180;
    Best Local Similarity 100.0%; Pred. No. 0.027;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAPR 15
    |||||

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Db 48 AGAARASGPGGAPR 62

RESULT 10
AAB03154
ID AAB03154 standard; protein; 180 AA.
XX AC AAB03154;
XX DT 23-OCT-2000 (first entry)
XX DE Human oesophageal cancer-associated antigen NY-ESO-1.
XX KW Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen;
XX oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain;
XX antibody; diagnostic marker; drug delivery target.
XX OS Homo sapiens.
XX FH Key
FT Modified-site 7 Location/Qualifiers
FT Modified-site 9 /note= "Potential N-myristoylation site"
FT Modified-site 11 /note= "Potential N-myristoylation site"
FT Modified-site 11 /note= "Potential O-phosphorylation site"
FT Modified-site 98 /note= "Potential O-phosphorylation site"
FT Modified-site 134 /note= "Potential O-phosphorylation site"
FT Modified-site 138 /note= "Potential O-phosphorylation site"
FT Modified-site 152.172 /note= "Potential O-phosphorylation site"
FT Domain /note= "Potential transmembrane domain"
XX US6069233-A.
XX PN 30-MAY-2000.
XX PD 26-JAN-1998; 98US-00013150.
XX PF 03-OCT-1996; 96US-00725381.
XX PR (SLOK ) SLOAN KETTERING INST CANCER RES.
XX PA (CORR ) CORNELL RES FOUND INC.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Scanlan M, Gure AO, Chen Y, Tureci O, Sahin U, Pfreundschuh M;
XX Old LJ;
XX WPI; 2000-410880/35.
XX DR N-PSDB; AAA61483.
XX PT New isolated esophageal cancer-associated antigen useful as markers for
XX producing antibodies and as targets for identifying abnormal conditions,
XX e.g. infections and cancer.
XX PS Example 5; Fig 3; 9pp; English.
XX CC This sequence represents a human oesophageal cancer-associated antigen,
XX NY-ESO-1. The cDNA encoding this sequence was isolated from a cDNA
XX library prepared from a specimen of well-to-moderately differentiated
XX squamous cell cancer of the oesophagus. Expression analysis demonstrated
XX that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma
XX cell lines and in normal ovary and testis tissue, but not in normal
XX colon, kidney, liver or brain tissue. Analysis of the amino acid sequence
XX of the protein indicates that the protein has a transmembrane domain,
XX several N-myristoylation sites and O-phosphorylation sites and that it
XX contains antigenic sequences in the N-terminal half of the protein. The
XX antigen is useful as an immunogen when combined with an adjuvant, in both
XX precursor and post-translationally modified forms, and may be used to
XX generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic
XX marker for oesophageal cancer, and can be utilised as a marker for the

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CC targetted delivery of therapeutic agents to oesophageal cancer cells. It
 CC can also be used to generate diagnostic or therapeutic agents
 XX
 SQ Sequence 180 AA;

Query Match 100.0%; Score 78; DB 3; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAPR 15
 DB 48 AGAARASGPGGAPR 62

RESULT 11
 AAB69946
 ID AAB69946 standard; protein; 180 AA.

AC AAB69946;

DT 27-APR-2001 (first entry)

DE Human NY-ESO-1 protein.

XX Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
 KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
 KW non-small cell lung carcinoma; tumour status determination.

XX Homo sapiens.

OS WO200107917-A1.

PN 01-FEB-2001.

PD 14-JUL-2000; 2000WO-US019220.

PF 23-JUL-1999; 99US-00359503.

PR (LUDW-) LUDWIG INST CANCER RES.

PA (SLOK) SLOAN KETTERING INST CANCER RES.

PA (CORR) CORNELL RES FOUND INC.

XX Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;

XX WPI; 2001-182822/18.

DR N-PSDB; AAF58634.

XX Method useful for determining the status (e.g. progression, regression or
 PT stability of the disease) of a cancerous condition, involves determining
 PT the levels of NY-ESO-1 specific antibodies in a sample taken from a
 PT patient.

XX Example 5; Fig 3; 50pp; English.

XX The present sequence is human NY-ESO-1 protein. It is provided in a
 CC specification relating to a method for determining the status of a
 CC cancerous condition in a patient with a tumour that expresses NY-ESO-1.
 CC The method comprises assaying a sample taken from the patient for
 CC antibodies that specifically bind to the NY-ESO-1 and comparing the value
 CC obtained to a prior value obtained from assay of a prior sample taken
 CC from the patient. Any difference between the values is indicative of a
 CC change in status of the cancerous condition. The method is useful for
 CC determining whether a cancerous condition is progressing, regressing or
 CC remaining stable, in particular in patients receiving treatment for a
 CC carcinoma, adenocarcinoma, non-small cell lung carcinoma or bladder
 CC carcinoma

XX Sequence 180 AA;

Query Match 100.0%; Score 78; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAPR 15
 DB 48 AGAARASGPGGAPR 62

RESULT 12
 AAG67164
 ID AAG67164 standard; protein; 180 AA.

AC AAG67164;

DT 13-NOV-2001 (first entry)

XX Amino acid sequence of cancer testis tumour antigen NY-ESO-1.

XX Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
 KW HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour;
 KW cancer; testis tumour.

XX Homo sapiens.

OS WO200162917-A1.

PN 30-AUG-2001.

PD 22-JAN-2001; 2001WO-US002126.

PF 22-FEB-2000; 2000US-00510635.

PR (LUDW-) LUDWIG INST CANCER RES.

PA Lethe B, Boon-Falleur T;

PI WPI; 2001-550091/61.

DR N-PSDB; AAH75118.

XX Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful
 PT for diagnosing testicular tumors.

XX Example 5; Fig 3; 50pp; English.

XX The present sequence represents cancer testis tumour antigen NY-ESO-1
 CC (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at
 CC least one human leukocyte antigen (HLA) binding peptide, which binds to
 CC Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is
 CC expressed in tumour mRNA and in testis, but not normal colon, kidney,
 CC liver or brain tissue. The presence or level of expression of NY-ESO-1
 CC may be assayed for the diagnosis of cancer, especially testis tumours

XX Sequence 180 AA;

Query Match 100.0%; Score 78; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAPR 15
 DB 48 AGAARASGPGGAPR 62

RESULT 13
 AAU01535
 ID AAU01535 standard; protein; 180 AA.

AC AAU01535;

DT 18-JUL-2001 (first entry)

DE Human NY-ESO-1 tumour rejection antigen precursor protein.

XX NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
 KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
 KW human leukocyte antigen-determining region; disease progression;

KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.

XX OS Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 7

FT Modified-site /note= "Myristoylated"

FT Modified-site 9

FT Modified-site /note= "Myristoylated"

FT Modified-site 11

FT Modified-site /note= "Phosphorylated"

FT Modified-site ,98

FT Modified-site /note= "Phosphorylated"

FT Modified-site 134

FT Modified-site /note= "Phosphorylated"

FT Modified-site 138

FT Modified-site /note= "Phosphorylated"

XX WO200123560-A2.

PN 05-APR-2001.

XX 26-SEP-2000; 2000WO-US026411.

XX 29-SEP-1999; 99US-00408036.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Tureci O, Sahin U, Pfreundschuh M;

XX WPI; 2001-266156/27.

XX N-PSDB; AAS02254.

XX Polypeptides binding to major histocompatibility complex class II human
XX leukocyte antigen-determining region molecule having amino acid sequence
XX found in tumor rejection antigen precursor used for stimulating
XX proliferation of helper T cells.
XX Claim 4; Fig 3; 62pp; English.

XX The sequence represents a human NY-ESO-1 tumour rejection antigen
XX precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to
XX major histocompatibility complex (MHC) Class II molecules such as human
XX leukocyte antigen-determining region (HLA-DR) molecules and stimulate
XX proliferation of helper T cells. The peptides can be administered to an
XX HLA-DR positive subject in order to stimulate the helper T cells. An MHC
XX Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell
XX or present in free form is useful for this stimulation. The nucleic acid
XX is useful for screening for a cancerous condition, which involves
XX contacting a subject sample to a cell line transfected with the
XX immunoreactive cell (helper T cell), where interaction is indicative of
XX cancer. In addition, a sample from a patient (for example, a body fluid
XX or tissue) can be monitored for the amount of the complex present in the
XX bloodstream. This is useful for determining regression, progression or
XX onset of a cancerous condition. The method involves contacting the sample
XX with a radioactive labelled or enzyme labelled monoclonal antibody which
XX specifically binds with the complex

XX Sequence 180 AA;

Query Match 100.0%; Score 78; DB 4; Length 180;

Best Local Similarity 100.0%; Pred. No. 0.027;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGAARASGPGGAPR 15

|||||

Db 48 AGAARASGPGGAPR 62

RESULT 14

AAE07714

ID AAE07714 standard; protein; 180 AA.

XX AAE07714;

XX 06-NOV-2001 (first entry)

XX Human NY ESO-1 protein.

XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.

XX OS Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 45. .47

XX /note= "Encoded by CCGGGGC"

XX WO200155393-A2.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US002765.

XX 28-JAN-2000; 2000US-0179004P.

XX 29-SEP-2000; 2000US-0237107P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang R, Rosenberg SA, Zeng G;

XX WPI; 2001-496851/54.

XX N-PSDB; AAD14179, AAD14180.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
XX useful as immunogen and vaccine for inhibiting cancer in a mammal or as
XX protection from metastasis.
XX Example 1; Fig 1; 134pp; English.

XX The invention relates to the identification and isolation of major
XX histocompatibility (MHC) class II restricted T cell epitope (MHC-II
XX epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
XX from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
XX antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
XX restricted. The products of the gene are promising candidates for
XX immunotherapeutic strategies for the prevention, treatment and diagnosis
XX of patients with cancer. The cancer epitopes are useful as immunogen and
XX vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
XX lymphocytes resulting in protection of the recipient from development of
XX cancer and protection from metastasis, or by inhibiting the growth of
XX cells expressing the NY-ESO-1 gene product. The cancer peptides are also
XX useful as diagnostic agent to detect the presence of cancer, to enhance
XX the generation of antibody and/or CD8+ T cell responses against any given
XX target antigen and/or hapten and to induce tumour-specific humoral-
XX mediated immunity against cancer. The present sequence is human NY ESO-1
XX protein

XX Sequence 180 AA;

Query Match 100.0%; Score 78; DB 4; Length 180;

Best Local Similarity 100.0%; Pred. No. 0.027;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGAARASGPGGAPR 15

|||||

Db 48 AGAARASGPGGAPR 62

RESULT 15

AAU84818

ID AAU84818 standard; protein; 180 AA.

```

XX AC AAU84818;
XX DT 08-MAY-2002 (first entry)
XX DE Human NYNSOLA consensus sequence.
XX KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
XX KW viral infection; human immunodeficiency virus; melanoma;
XX KW bacterial infection; Salmonella; Legionella; parasitic infection;
XX KW Trypanosoma; Toxoplasma; Giardia.
XX OS Homo sapiens.
XX PN WO200190197-A1.
XX PD 29-NOV-2001.
XX PF 25-MAY-2001; 2001WO-AU000622.
XX PR 26-MAY-2000; 2000AU-00007761.
XX PA (AUSU ) UNIV AUSTRALIAN NAT.
XX PI Thomson SA, Ramshaw IA;
XX DR WPI; 2002-147575/19.
XX PT New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX PS Example 3; Fig 27; 364pp; English.
XX CC The invention relates to a new synthetic polypeptide (1) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a consensus sequence for a parent protein used to design a savine of the
CC invention
XX SQ Sequence 180 AA;
Query Match 100.0%; Score 78; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGAARASGPGGAPR 15
Db 48 AGAARASGPGGAPR 62

```

Search completed: March 13, 2006, 19:03:59
 Job time : 113.941 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:04:24 ; Search time 17,8235 Seconds
(without alignments)
80.975 Million cell updates/sec

Title: US-09-529-206E-26
Perfect score: 78
Sequence: 1 AGAARASGPGGAPR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	64.1	82	T04476	acclimation protei
2	50	64.1	222	T36115	probable oxidoredu
3	49	62.8	351	S50754	hypothetical prote
4	48.5	62.2	566	T21096	hypothetical prote
5	48.5	62.2	692	T21095	hypothetical prote
6	48	61.5	220	T27464	hypothetical prote
7	48	61.5	1690	T35894	ATP dependent DNA
8	47	60.3	380	JC1451	Ca2+/calmodulin-de
9	46	59.0	333	C48423	homeotic protein e
10	46	59.0	504	AE3526	5-carboxymethyl-2-
11	45	57.7	173	AB3648	flagellar basal-bo
12	45	57.7	275	C84673	hypothetical prote
13	45	57.7	627	A44112	spidroin 2, dragli
14	45	57.7	651	A36333	dnak-type molecula
15	44.5	57.1	335	S08341	myristylated alani
16	44.5	57.1	730	A36226	collagen alpha 1 c
17	44	56.4	226	S51660	histone H1-5 [vali
18	44	56.4	232	1 TVPV10	transforming prote
19	44	56.4	259	A44988	transforming prote
20	44	56.4	269	A47008	transcription acti
21	44	56.4	286	S04673	H+-transporting tw
22	44	56.4	305	A49011	c-Crk - chicken
23	44	56.4	309	1 A39169	myristylated alani
24	44	56.4	379	1 A48082	MAP kinase 3 (EC 2
25	44	56.4	510	2 A42750	insulinoma-associ
26	44	56.4	679	2 S02165	regulatory protein
27	44	56.4	900	2 B70694	probable infB - My
28	44	56.4	924	2 F87103	initiation factor
29	44	56.4	954	2 A87431	regulatory protein

30	44	56.4	1134	2 A41350	adenylate cyclase
31	44	56.4	3190	2 T13828	CREB-binding prote
32	43.5	55.8	328	2 A44192	heterogeneous nucl
33	43	55.1	185	2 T36874	hypothetical prote
34	43	55.1	189	2 AE3136	hypothetical prote
35	43	55.1	189	2 G98151	hypothetical prote
36	43	55.1	213	2 S42585	DNA-invertase - Rh
37	43	55.1	260	2 T32525	hypothetical prote
38	43	55.1	280	2 D70803	hypothetical prote
39	43	55.1	307	2 B72677	hypothetical prote
40	43	55.1	341	2 JC4051	jun-D protein - ra
41	43	55.1	349	2 S55626	hypothetical prote
42	43	55.1	377	2 S28184	Ca2+/calmodulin-de
43	43	55.1	420	2 A49642	transcription fact
44	43	55.1	431	2 E82766	conserved hypochet
45	43	55.1	437	2 T30220	membrane transport

ALIGNMENTS

RESULT 1

T04476

acclimation protein 2 - barley

C;Species: Hordeum vulgare (barley)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T04476

R;Phillips, J.R.; Dunn, M.A.; Hughes, M.A.

Plant Mol. Biol. 33, 1013-1023, 1997

A;Title: mRNA stability and localisation of the low temperature responsive barley gene

A;Reference number: Z15367; MUID:97299834; PMID:9154983

A;Accession: T04476

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-82 <PHI>

A;Cross-references: UNIPROT:Q40033; UNIPARC:UPI000009CE5A; EMBL:X97917; NID:G1418969; P

A;Experimental source: cv. Igri

C;Genetics:

A;Gene: blt14.2

Query Match 64.1%; Score 50; DB 2; Length 82;
Best Local Similarity 69.2%; Pred. No. 4.6;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAARASGPGGAP 14

DB 31 GAARGAGAGGVP 43

RESULT 2

T36115

probable oxidoreductase - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004

C;Accession: T36115

R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, April 1999

A;Reference number: Z21597

A;Accession: T36115

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-222 <MUR>

A;Cross-references: UNIPROT:Q9X887; UNIPARC:UPI00000DB008; EMBL:AL049707; PTDN:CAB41281

A;Experimental source: strain A3(2)

C;Genetics:

A;Gene: SCOEDB:SCE15.12c

C;Superfamily: NAD(P)H-dependent FMN reductase (sulfate starvation-induced protein 4);

Query Match 64.1%; Score 50; DB 2; Length 222;

Best Local Similarity 64.3%; Pred. No. 11;

Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAP 14

RESULT 8

JC1451
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) - rat
N;Alternate names: ERK1-MAP kinase; extracellular signal-regulated kinase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JC1451; A35061; A37140; A40466; S24947
R;Marquardt, B.; Stabel, S.
Gene 120, 297-299, 1992
A;Title: Sequence of a rat cDNA encoding the ERK1-MAP kinase.
A;Reference number: JC1451; MUID:93013050; PMID:1327976
A;Accession: JC1451;
A;Molecule type: mRNA
A;Residues: 1-380 <MAR>
A;Cross-references: UNIPROT:P21708; UNIPARC:UPI000012F174; EMBL:X651198; NID:G56626; PIDN:
A;Experimental source: brain
R;Boulton, T.G.; Yancopoulos, G.D.; Gregory, J.S.; Slaughter, C.; Moomaw, C.; Hsu, J.; Q
Science 249, 64-67, 1990
A;Title: An insulin-stimulated protein kinase similar to yeast kinases involved in cell
A;Reference number: A35061; MUID:90312137; PMID:2164259
A;Accession: A35061
A;Molecule type: mRNA
A;Residues: 14-380 <BOU>
A;Cross-references: UNIPARC:UPI0000145072; GB:M381194; NID:G204051; PIDN:AAA41123.1; PID:
R;Boulton, T.G.; Gregory, J.S.; Cobb, M.H.
Biochemistry 30, 278-286, 1991
A;Title: Purification and properties of extracellular signal-regulated kinase 1, an insu
A;Reference number: A37140; MUID:91105092; PMID:1846291
A;Accession: A37140
A;Status: preliminary
A;Molecule type: protein
A;Residues: 43-64;167-178,'X',180-183,'X',185 <BO2>
A;Cross-references: UNIPARC:UPI000017558F; UNIPARC:UPI0000175590
R;De Miguel, C.; Kligman, D.; Patel, J.; Deterra-Wadleigh, S.D.
DNA Cell Biol. 10, 505-514, 1991
A;Title: Molecular analysis of microtubule-associated protein-2 kinase cDNA from mouse a
A;Reference number: A40466; MUID:91369479; PMID:1716439
A;Accession: A40466
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 14-94,'R',96-380 <DEM>
A;Cross-references: UNIPARC:UPI00001707C5; GB:U12008; GB:S59509; NID:G515498; PIDN:AAA20
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; calmodulin binding; phosphoprotein; phosphotransferase; serine/threonin
F;41-331/Domain: protein kinase homology <KIN>
F;49-57/Region: protein kinase ATP-binding motif

Query Match 60.3%; Score 47; DB 2; Length 380;
Best Local Similarity 66.7%; Pred. No. 42;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAPR 15
Db 2 AAAAAAPGGGGGPR 16

RESULT 9

C48423
homeotic protein engrailed 1 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
C;Accession: C48423
R;Logan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, D.; Provart, N.J.; Joyner, A.I
Dev. Genet. 13, 345-358, 1992
A;Title: Cloning and sequence comparison of the mouse, human, and chicken engrailed gene
A;Reference number: A48423; MUID:93185339; PMID:1363401
A;Accession: C48423
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-333 <LOG>
A;Cross-references: UNIPARC:UPI000017A297
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;245-301/Domain: homeobox homology <HOX>

Query Match 59.0%; Score 46; DB 2; Length 333;
Best Local Similarity 64.3%; Pred. No. 51;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAP 14
Db 166 AGAAKAQGDGETP 179

RESULT 10

AE3526
5-carboxymethyl-2-hydroxy-muconate semialdehyde dehydrogenase (EC 1.2.1.1-) [imported] -
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AE3526
R;DelVecchio, V.G.; Kapratl, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagijs, S.; O'Callaghan, D.; Letes
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten
A;Reference number: AD3252; PMID:11756688
A;Accession: AE3526
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-504 <KUR>
A;Cross-references: UNIPROT:Q8YDPO; UNIPARC:UPI0000058376; GB:AE008918; PIDN:AAL53376.1
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BME110135
A;Map position: II
C;Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology
C;Keywords: oxidoreductase

Query Match 59.0%; Score 46; DB 2; Length 504;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAARASGPGGG 12
Db 366 AGGAKFAGPGGG 377

RESULT 11

AB3648
flagellar basal-body rod protein flgF [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AB3648
R;DelVecchio, V.G.; Kapratl, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagijs, S.; O'Callaghan, D.; Letes
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten
A;Reference number: AD3252; PMID:11756688
A;Accession: AB3648
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <KUR>
A;Cross-references: UNIPROT:Q8YAZ4; UNIPARC:UPI0000058740; GB:AE008918; PIDN:AAL54349.1
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BME11107
A;Map position: II

Query Match 57.7%; Score 45; DB 2; Length 173;
Best Local Similarity 64.3%; Pred. No. 39;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GAARASGPGGGAPR 15
Db 125 GAPIVLNPGGGAPR 138

RESULT 12

C84673
 hypothetical protein At2g27470 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: C84673
 R:Lin. X.; Kaul, S.; Rounslev, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, A.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: C84673
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-275 <STO>
 A:Cross-references: UNIPROT:Q9ZQH2; UNIPARC:UPI000000C26F; GB:AE002093; NID:G4314389; PID:Q9ZQH2
 C:Genetics:
 A:Gene: At2g27470
 A:Map position: 2

Query Match 57.7%; Score 45; DB 2; Length 275;
 Best Local Similarity 76.9%; Pred. No. 59;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAARASGPGGA 13
 ||||| |||||
 DB 107 AGAAAASYPAGGA 119

RESULT 13
 A44112
 spider2, dragline silk fibroin - orb spider (Nephila clavipes) (fragment)
 N:Alternate names: silk fibroin, dragline
 C:Species: Nephila clavipes
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: A44112; S27824
 R:Hinman, M.B.; Lewis, R.V.
 J. Biol. Chem. 267, 19320-19324, 1992
 A:Title: Isolation of a clone encoding a second dragline silk fibroin. Nephila clavipes
 A:Reference number: A44112; MUID:92406876; PMID:1527052
 A:Accession: A44112
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-627 <H12>
 A:Cross-references: UNIPROT:P46804; UNIPARC:UPI0000135DC6; GB:M92913; NID:gl59713; PID:G4314389
 A:Note: sequence extracted from NCBI backbone (NCBIP:113893)
 R:Hinman, M.B.; Lewis, R.V.
 submitted to the EMBL Data Library, May 1992
 A:Description: Isolation of a clone encoding a second dragline silk fibroin: Nephila clavipes
 A:Reference number: S27824

A:Accession: S27824
 A:Molecule type: mRNA
 A:Residues: 19-627 <H12>
 A:Cross-references: UNIPARC:UPI000017BE0B; EMBL:M92913

Query Match 57.7%; Score 45; DB 2; Length 627;
 Best Local Similarity 64.3%; Pred. No. 1.2e+02;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAP 14
 ||||| |||||
 DB 30 AAAAAGGPGGVP 43

RESULT 14
 A36333
 dnaK-type molecular chaperone Hsc70-4 - fruit fly (Drosophila melanogaster)
 N:Alternate names: heat shock cognate protein 70
 C:Species: Drosophila melanogaster
 C:Date: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 31-Dec-2004
 C:Accession: A36333
 R:Perkins, L.A.; Doctor, J.S.; Zhang, K.; Stinson, L.; Perrimon, N.; Craig, E.A.
 Mol. Cell. Biol. 10, 3232-3238, 1990

A:Title: Molecular and developmental characterization of the heat shock cognate 4 gene
 A:Reference number: A36333; MUID:90258915; PMID:2111451
 A:Accession: A36333
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-651 <PER>
 A:Cross-references: UNIPROT:P11147; UNIPARC:UPI000016BC3E; GB:M36114; NID:gl57663; PID:N36114
 C:Genetics:
 A:Gene: FlyBase:Hsc70-4
 A:Cross-references: FlyBase:FBgn0001219
 C:Function:
 A:Description: involved in protein folding and assembling/disassembling of protein complex
 C:Superfamily: bcr protein
 C:Keywords: ATP; molecular chaperone; nucleus

Query Match 57.7%; Score 45; DB 2; Length 651;
 Best Local Similarity 64.3%; Pred. No. 1.2e+02;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAP 14
 ||||| |||||
 DB 632 AGAAGAGGAGGAP 645

RESULT 15
 S08341
 myristylated alanine-rich protein kinase C substrate - bovine
 N:Alternate names: acidic calmodulin-binding 81K protein (ACAMP-81); MARCKS
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
 C:Accession: S08341; A32904; S29270; A46098; PS0338
 R:Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
 Nucleic Acids Res. 17, 3987-3988, 1989
 A:Title: Nucleotide sequence of a cDNA for the bovine myristoylated alanine-rich C kinase
 A:Reference number: S08341; MUID:89282412; PMID:2734111
 A:Accession: S08341
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-335 <STU>
 A:Cross-references: UNIPROT:P12624; UNIPARC:UPI000016C340; EMBL:M24638; NID:gl63339; PID:P12624
 R:Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
 Proc. Natl. Acad. Sci. U.S.A. 86, 4012-4016, 1989
 A:Title: Molecular cloning, characterization, and expression of a cDNA encoding the "80-
 A:Reference number: A32904; MUID:89264553; PMID:2726763

A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-98,'Q','100-335 <ST2>
 A:Cross-references: UNIPARC:UPI000017750A; GB:M24638; GB:M23738
 R:Herget, T.; Brooks, S.F.; Broad, S.; Rozengurt, E.
 Eur. J. Biochem. 209, 7-14, 1992
 A:Title: Relationship between the major protein kinase C substrates acidic 80-kDa protein
 or equivalent genes in different species.
 A:Reference number: S29267; MUID:93011168; PMID:1396720

A:Accession: S29270
 A:Molecule type: DNA
 A:Residues: 191-253,'SEE',257-279,283-292,'V',294,'PEQE',299,'A',300,'A',302-313,'A',315
 A:Cross-references: UNIPARC:UPI000017750B
 R:Manenti, S.; Sorokine, O.; Van Dorsselelaer, A.; Taniguchi, H.
 J. Biol. Chem. 268, 6878-6881, 1993
 A:Title: Isolation of the non-myristoylated form of a major substrate of protein kinase
 A:Reference number: A46098; MUID:93216617; PMID:8463217

A:Accession: A46098
 A:Molecule type: protein
 A:Residues: 2-11 <MAN>
 A:Cross-references: UNIPARC:UPI000017750C
 R:Mizutani, A.; Tokumitsu, H.; Hidaka, H.
 Biochem. Biophys. Res. Commun. 182, 1395-1401, 1992
 A:Title: Acidic calmodulin binding protein, ACAMP-81, is MARCKS protein interacting with
 A:Reference number: PS0338; MUID:92171958; PMID:1540183
 A:Accession: PS0338
 A:Molecule type: protein
 A:Residues: 12-30,56-69,88-98,'AS',100-103,104-109,'E',111-123,156-160;165-171,196-215;2

A;Cross-references: UNIPARC:UPI000017750D; UNIPARC:UPI000017750E; UNIPARC:UPI000017750F;
514
A;Experimental source: brain
A;Note: this sequence is identical with that of myristoylated alanine-rich C-kinase sub
C;Comment: This protein is a major cellular substrate for protein kinase C and plays a r
C;Comment: It binds to calmodulin in one to one molar ratio in the presence of calcium a
C;Genetics:
A;Introns: 34/3
C;Superfamily: neurofilament triplet H protein
C;Keywords: actin binding; blocked amino end; calmodulin binding; lipoprotein; myristyla
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;158,162,166,169/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
Query Match 57.1%; Score 44.5; DB 2; Length 335;
Best Local Similarity 54.2%; Pred. No. 81;
Matches 13; Conservative 1; Mismatches 1; Indels 9; Gaps 2;
Qy 1 AGAA-----RASGFG----GGAPR 15
Db 278 AGAAGCEAPSAAGGCGCPRAGGAPR 301

Search completed: March 13, 2006, 19:16:10
Job time : 19.8235 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 18:53:23 ; Search time 108.882 Seconds
(without alignments)
97.196 Million cell updates/sec

Title: US-09-529-206E-26
Perfect score: 78
Sequence: 1 AGAARASGPGGAPR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	142	Q9NY13_HUMAN	Q9ny13 homo sapien
2	78	100.0	180	CTG1B_HUMAN	P78358 homo sapien
3	78	100.0	180	Q7LBY4_HUMAN	Q7lby4 homo sapien
4	70	89.7	210	CTAG2_HUMAN	P75638 homo sapien
5	55	70.5	337	CT086_HUMAN	Q9bz19 homo sapien
6	55	70.5	559	Q8L680_ORYSA	Q8l680 oryza sativ
7	55	70.5	867	Q94LD1_ORYSA	Q94ld1 oryza sativ
8	54	69.2	362	Q63OT8_BURPS	P63ct8 burkholderi
9	54	69.2	362	Q62H22_BURMA	P62h22 burkholderi
10	54	69.2	895	Q4NUK4_9DELT	Q4nuk4 anaeromyxob
11	53	67.9	321	Q96S27_HUMAN	Q96s27 homo sapien
12	53	67.9	322	Q67PJ0_SYMPH	P67pj0 symbiobacte
13	53	67.9	644	Q688J5_ORYSA	Q688j5 oryza sativ
14	53	67.9	1379	Q7QK55_ANOGA	Q7qk55 anopheles g
15	52.5	67.3	924	Q4NOS2_9DELT	Q4nq82 anaeromyxob
16	52	66.7	447	Q4GRAS_9RBI	Q9gras gryllus blm
17	52	66.7	786	Q4QCF3_LEINA	Q4qcf3 leishmania
18	52	66.7	3288	Q7TSD9_CHV1	P7t5d9 cercopithe
19	52	66.7	3326	Q7T591_CHV1	P7t591 cercopithe
20	51	65.4	367	Q6AV33_ORYSA	P6av33 oryza sativ
21	51	65.4	405	Q4JWB8_CORJK	P4jwb8 corynebacte
22	51	65.4	472	Q5C8R1_9ADEN	Q5c8r1 simian aden
23	51	65.4	880	Q63K38_BURPS	P63k38 burkholderi
24	51	65.4	926	CEZ2_MOUSE	P8r554 mus musculu
25	51	65.4	1031	Q75IL4_ORYSA	Q75il4 oryza sativ
26	50.5	64.7	108	Q8H321_ORYSA	Q8h321 oryza sativ
27	50	64.1	82	Q40033_HORVU	P40033 hordeum vul
28	50	64.1	102	Q4R9N8_TETNG	Q4r9n8 tetraodon n
29	50	64.1	111	Q5NTAS_CANFA	P5ntas canis faml
30	50	64.1	194	Q96BU2_HUMAN	P96bu2 homo sapien
31	50	64.1	222	Q9X887_STRCO	P9x887 streptomyce

32	50	64.1	341	2	Q6H6A6_ORYSA	Q6h6a6 oryza sativ
33	50	64.1	550	2	Q86P11_TOXGO	Q86p11 toxoplasma
34	50	64.1	896	2	Q96D18_HUMAN	Q96d18 homo sapien
35	50	64.1	1253	2	Q6DRV6_HUMAN	Q6drv6 homo sapien
36	50	64.1	1430	2	Q9H7P9_HUMAN	Q9h7p9 homo sapien
37	50	64.1	1787	2	Q9M4X9_CHLRE	Q9m4x9 chlamydomon
38	49.5	63.5	835	1	NLGN2_HUMAN	Q8nfz4 homo sapien
39	49.5	63.5	836	1	NLGN2_RAT	Q82888 rattus norv
40	49.5	63.5	836	2	O5F285_MOUSE	Q5f288 mus musculu
41	49.5	63.5	884	2	Q69ZK9_MOUSE	Q69zk9 mus musculu
42	49	62.8	160	2	Q94LU4_ORYSA	Q94lu4 oryza sativ
43	49	62.8	172	2	Q9DCH0_MOUSE	Q9dch0 mus musculu
44	49	62.8	175	1	PACA_CHICK	P41534 g glucagon-
45	49	62.8	327	2	Q63HT9_BURPS	Q63ht9 burkholderi

ALIGNMENTS

RESULT 1

Q9NY13_HUMAN	PRELIMINARY;	PRT;	142 AA.
AC	Q9NY13;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)		
DE	Hypothetical protein LAGE-2 (Fragment).		
GN	Name=LAGE-2;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Lethe B.G.;		
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ275978; CAB76945.1; -; mRNA.		
KW	Hypothetical protein.		
FT	NON_TER 1		
SQ	SEQUENCE 142 AA; 13895 MW; 27BBE922AC4ACC7B CRC64;		

Query Match 100.0%; Score 78; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY	1	AGAARASGPGGAPR 15	
DB	22	AGAARASGPGGAPR 36	

RESULT 2

CTG1B_HUMAN	STANDARD;	PRT;	180 AA.
ID	CTG1B_HUMAN		
AC	P78358;		
DT	15-DEC-1998 (Rel. 37, Created)		
DT	15-DEC-1998 (Rel. 37, Last sequence update)		
DT	10-MAY-2005 (Rel. 47, Last annotation update)		
DE	Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-ESO-1).		
DE	GN		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RX	MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;		
RA	Chen Y.-T., Scantlan M.J., Sahin U., Tuerci O., Gure A.O., Tsang S.,		
RA	Williamson B., Stockert E., Pfrendrich M., Old L.J.;		
RT	"A testicular antigen aberrantly expressed in human cancers detected by autologous antibody screening."		

```

FL Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918 (1997).
FN [2]
FP NUCLEOTIDE SEQUENCE.
FC TISSUE=Melanoma;
RX MEDLINE=98289662; PubMed=9626360;
RA Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA de Plaen E., Boon T.;
RT "LAGE-1, a new gene with tumor specificity.";
RL Int. J. Cancer 76:903-908 (1998).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98430682; PubMed=9759882;
RA Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,
RA Schwartzentruber D.J., Rosenberg S.A.;
RT "A breast and melanoma-shared tumor antigen: T cell responses to
RT antigenic peptides translated from different open reading frames.";
RL J. Immunol. 161:3596-3606 (1998).
CC -!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide
CC variety of cancers. Detected in uterine myometrium.
CC -!- SIMILARITY: Belongs to the CTAG family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC -----
DR EMBL; U87459; AAB49693.1; -; mRNA.
DR EMBL; AJ003149; CA005908.1; -; mRNA.
DR EMBL; AF038567; AAD05202.1; -; mRNA.
DR HGNC; HGNC:2491; CTAG1B.
DR MIM; 300156; -.
KW Antigen; Transmembrane.
FT TRANSMEM 156 172 Potential.
FT COMPIAS 5 82 Gly-rich.
SQ SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;

Query Match 100.0%; Score 78; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAPR 15
DB 48 AGAARASGPGGGAPR 62

RESULT 3
Q7LBY4 HUMAN
ID Q7LBY4_HUMAN PRELIMINARY; PRT; 180 AA.
AC Q7LBY4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
DE antigen 1-A).
GN Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21303268;
RA Galgoczy P., Rosenthal A., Platzer M.;
RT "Human-mouse comparative sequence analysis of the NEMO gene reveals an
RT alternative promoter within the neighboring G6PD gene.";
RL Gene 271:93-98 (2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21566154; PubMed=11709543; DOI=10.1093/hmg/10.22.2557;
RA Aradhy S., Bardaro T., Galgoczy P., Yamagata T., Deposito T.,
RA Patlan H., Ciccodicola A., Kenwick S., Platzer M., D'Urso M.,

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RA Nelson D.L.;
RT "Multiple pathogenic and benign genomic rearrangements occur at a 35
RT kb duplication involving the NEMO and LAGE2 genes.";
RL Hum. Mol. Genet. 10:2557-2567 (2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Platzer M.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Platzer M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Galgoczy P., Platzer M.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99454989; PubMed=10523621;
RA De Smet C., Durquin C., Lethe B., Martelange V., Boon T.;
RT "DNA methylation is the primary silencing mechanism for a set of germ
RT line- and tumor-specific genes with a CpG-rich promoter.";
RL Mol. Cell. Biol. 19:7327-7335 (1999).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF277315; AAL27014.1; -; Genomic DNA.
DR EMBL; AJ275977; CAB76943.1; -; Genomic DNA.
DR EMBL; AF277315; AAL27013.1; -; Genomic DNA.
SQ SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;

Query Match 100.0%; Score 78; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAPR 15
DB 48 AGAARASGPGGGAPR 62

RESULT 4
CTAG2 HUMAN
ID CTAG2_HUMAN STANDARD; PRT; 210 AA.
AC Q75638; Q75637; Q9UB80; Q9UJ99; Q9Y479;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
GN Name=CTAG2; Synonyms=ESO2, LAGE1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B).
RC TISSUE=Melanoma;
RX MEDLINE=98289662; PubMed=9626360;
RA Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA de Plaen E., Boon T.;
RT "LAGE-1, a new gene with tumor specificity.";
RL Int. J. Cancer 76:903-908 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B), AND VARIANTS
RP GLN-6; GLN-89 AND ARG-138.
RC TISSUE=Melanoma;
RX MEDLINE=99325550; PubMed=10399963;
RA Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT unexpected translation product of LAGE-1.";
RL Int. J. Cancer 82:442-448 (1999).
RN [3]

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Qy 1 AGAARASGPGGGAPR 15
| | | | | | | | | |
Db 48 AGAARASGPRGGAPR 62

RESULT 5

CT086_HUMAN	STANDARD;	PRT;	337 AA.
AC Q9BZ19;			
28-FEB-2003 (Rel. 41, Created)			
28-FEB-2003 (Rel. 41, Last sequence update)			
10-MAY-2005 (Rel. 47, Last annotation update)			
DT Hypothetical protein C20orf86.			
DE Name=C20orf86;			
GN Homo sapiens (Human).			
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RX MEDLINE:21638749; PubMed:11780052; DOI=10.1038/414865a;			
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,			
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,			
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,			
RA Baileys O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,			
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,			
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,			
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,			
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,			
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,			
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,			
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,			
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,			
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,			
RA Leharshlaib M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,			
RA Marsh V.L., Martin S.L., McConnachie I.J., McClay K., McMurray A.A.,			
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,			
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,			
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,			
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,			
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,			
RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,			
RA Tracey A., Tsymans A.C., Vaudin M., Wall M., Wallis J.M.,			
RA Whitehead S.L., Whitcaker P., Willey D.L., Williams L., Williams S.A.,			
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,			
RA Rogers J.;			
RT "The DNA sequence and comparative analysis of human chromosome 20.";			
RL Nature 414:865-871(2001).			
CC -1- SIMILARITY: Contains 2 ANK repeats.			
CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.			
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CC use as long as its content is in no way modified and this statement is not			
CC removed.			
CC -----			
DR EMBL; AL354776; CAC17565.2; -; Genomic DNA.			
DR HSSP; P42771; 2A5E.			
DR Ensembl; ENSG00000124227; Homo sapiens.			
DR HGNC; HGNC:16217; C20orf86.			
DR InterPro; IPR002110; ANK.			
DR InterPro; IPR000626; Ubiquitin.			
DR Pfam; PF00023; ANK; 2.			
DR PRINTS; PR01415; ANKYRIN.			
DR SMART; SM00248; ANK; 2.			
DR PROSITE; PS50297; ANK REP REGION; 1.			
DR PROSITE; PS50088; ANK REPEAT; 2.			
DR PROSITE; PS500299; UBIQUITIN 1; FALSE NEG.			
DR PROSITE; PS50053; UBIQUITIN 2; 1.			
KW ANK repeat; Hypothetical protein; Polymorphism; Repeat.			

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FT DOMAIN      88      164      Ubiquitin-like.
FT REPEAT      211     241
FT REPEAT      244     273      ANK 1.
FT VARIANT      287     287      R -> C (in dbSNP:584855) .
FT             /FTId=VAR_014400.
SQ SEQUENCE    337 AA; 36714 MW; EC8BA4AD414756CB CRC64;

Query Match      70.5%; Score 55; DB 1; Length 337;
Best Local Similarity 73.3%; Pred. No. 27;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAPR 15
   |||||
DB 8 AGGARAAGTGGASR 22

RESULT 6
Q8L680_ORYSA
ID Q8L680_ORYSA PRELIMINARY; PRT; 559 AA.
AC Q8L680;
CT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Hypothetical protein OSJNBa0011L09.12.
EN ORFNames=OSJNBa0011L09.12;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
RA Jin S.S., Koo H., Zismann V., Heiao J., Blunt S., Vanaken S.S.,
RA Uterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA Peterson J.T., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Yuan Q., Ouyang S., Hill J.N., Gansberger K.,
RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,
RA Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., Vanaken S.E.,
RA Uterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
RA White O., Fraser C.M.;
RA Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC094404; AAK50601.1; -; Genomic_DNA.
DR Gramene; Q94LD1; -.
DR InterPro; IPR007228; DUF390.
DR InterPro; IPR007321; Transposase_28.
DR Pfam; PF04094; DUF390; 3.
DR Pfam; PF04195; Transposase_28; 1.
KW Hypothetical protein.
SQ SEQUENCE    867 AA; 92812 MW; 7365009715EDDC21 CRC64;

Query Match      70.5%; Score 55; DB 2; Length 867;
Best Local Similarity 66.7%; Pred. No. 63;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAPR 15
   |||||
DB 205 AGGSRAGGPGGGSR 219

RESULT 8
Q83Q78_BURPS
ID Q83Q78_BURPS PRELIMINARY; PRT; 362 AA.
AC Q83Q78;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative DNA polymerase III.
GN Ordered locus names=BPSL2936;
OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; pseudomallei group.
OX NCBI_TaxID=28450;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K96243;
RX PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bacon N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Chervach I.,
RA Chillingworth T., Cronin A., Crosssett B., Davis P., Deshazer D.,
RA Fellwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitch E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilai S., Stevens K., Tumapa S., Vesaratchaveh M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RL Burkholderia pseudomallei."
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).
DR EMBL; BX571965; CAH36946.1; -; Genomic_DNA.

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DR GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR InterPro; IPR010372; DNA_pol3_delta.
DR InterPro; IPR005790; DNA_polIII_delta.
DR Pfam; PF06144; DNA_pol3_delta.1.
DR TIGRFAMs; TIGR01128; hoIA; 1.
KW Complete proteome.
SQ SEQUENCE 362 AA; 38726 MW; D5FF3DE783D41E41 CRC64;

Query Match 69.2%; Score 54; DB 2; Length 362;
Best Local Similarity 83.3%; Pred. No. 38;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ARASGPGGGAPR 15
   |||:|||||
   348 ARAAGFGGDAPR 359

Db

RESULT 9
Q62H22 BURMA
ID Q62H22 BURMA PRELIMINARY; PRT; 362 AA.
AC Q62H22
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE DNA polymerase III, delta subunit (BC 2.7.7.7).
GN Name:hoIA; OrderedLocNames=BMA2451;
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=13373;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 23344;
RX PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA Nierman W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA Daugherty S.C., Davidson T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA Madupu R., Mohammed Y., Nelson W.C., Radune D., Romero C.M.,
RA Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA Zaia N., Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR EMBL; CP000010; AAU49707.1; -; Genomic_DNA.
DR TIGR; BMA2451; -
DR GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR InterPro; IPR010372; DNA_pol3_delta.
DR InterPro; IPR005790; DNA_polIII_delta.
DR Pfam; PF06144; DNA_pol3_delta.1.
DR TIGRFAMs; TIGR01128; hoIA; 1.
KW Complete proteome; Nucleotidyltransferase; Transferase.
SQ SEQUENCE 362 AA; 38726 MW; D5FF3DE783D41E41 CRC64;

Query Match 69.2%; Score 54; DB 2; Length 362;
Best Local Similarity 83.3%; Pred. No. 38;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ARASGPGGGAPR 15
   |||:|||||
   348 ARAAGFGGDAPR 359

Db

RESULT 10
Q4NUK4_9DELTA
ID Q4NUK4_9DELTA PRELIMINARY; PRT; 895 AA.
AC Q4NUK4_9
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Liga.

```

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GN ORFNames=AdehDRAFT_2813;
OS Anaeromyxobacter dehalogenans 2CP-C.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cyctobacterineae; Myxococcaceae; Anaeromyxobacter.
OX NCBI_TaxID=290397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Anaeromyxobacter
RT dehalogenans 2CP-C.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Anaeromyxobacter
RT dehalogenans 2CP-C.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHD01000013; EAL79351.1; -; Genomic DNA.
SQ SEQUENCE 895 AA; 93871 MW; 0AE25BBBF172BDB0 CRC64;

Query Match 69.2%; Score 54; DB 2; Length 895;
Best Local Similarity 73.3%; Pred. No. 88;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAPR 15
   |||:|||||
   795 AAARRARGAGGGAPR 809

Db

RESULT 11
Q96S27 HUMAN
ID Q96S27_HUMAN PRELIMINARY; PRT; 321 AA.
AC Q96S27;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein gene X.
GN Name:gene X;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21096910; PubMed=11157797; DOI=10.1093/hmg/10.4.339;
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA Higgs D.R.;
RT "Sequence, structure and pathology of the fully annotated terminal 2
RT Mb of the short arm of human chromosome 16.";
RL Hum. Mol. Genet. 10:339-352(2001).
DR EMBL; AE006463; AAK61225.1; -; Genomic DNA.
DR Ensembl; ENSG0000167933; Homo sapiens.
KW Hypothetical protein.
SQ SEQUENCE 321 AA; 32979 MW; 9C8764CFA17F4CD4 CRC64;

Query Match 67.9%; Score 53; DB 2; Length 321;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAPR 15
   |||:|||||
   3 SAARRARGGGAPR 17

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RESULT 12
C67PJ0 SYMTH
ID Q67PJ0 SYMTH PRELIMINARY; PRT; 322 AA.
AC Q67PJ0;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Prephenate dehydrogenase.
GN OrderedLocusNames=STH1418;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IAM14863;
RX PubMed=15383646; DOI=10.1093/nar/gkh830;
RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsui T.,
  Morimura K., Ikeda H., Hattori M., Beppu T.;
  "Genome sequence of Symbiobacterium thermophilum, an uncultivable
  bacterium that depends on microbial commensalism.";
  RL Nucleic Acids Res. 32:4937-4944 (2004).
DR EMBL; AP006840; BAD40403.1; -; Genomic DNA.
DR GO; GO:0046655; F:prephenate dehydrogenase (NADP+) activity; IEA.
DR GO; GO:0006571; P:tyrosine biosynthesis; IEA.
DR InterPro; IPR003039; Prephen_dehydrog.
DR Pfam; PF02153; PDH; 1.
KW Complete proteome.
SQ SEQUENCE 322 AA; 32843 MW; 09A06AC0AFA734EC CRC64;

Query Match 67.9%; Score 53; DB 2; Length 322;
Best Local Similarity 84.6%; Pred. No. 47;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGA 13
Db |||||

RESULT 13
Q688J5 ORYSA
ID Q688J5 ORYSA PRELIMINARY; PRT; 644 AA.
AC Q688J5;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein OSUNBB0012G21.2.
GN Names=OSUNBB0012G21.2;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
  Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
  Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
  Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C.,
  Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
  Wu H.-P., Shaw J.-P.;
  "Oryza sativa BAC OSUNBB0012G21 genomic sequence.";
  RT Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC135421; AAU01755.1; -; Genomic DNA.
DR Gramene; Q688J5; -
DR GO; GO:004057; F:arginyltransferase activity; IEA.
DR GO; GO:0016598; P:protein arginylation; IEA.
DR GO; GO:0042176; P:regulation of protein catabolism; IEA.
DR InterPro; IPR007472; ATE C.
DR InterPro; IPR007471; ATE N.
DR Pfam; PF04377; ATE C; 1.
DR Pfam; PF04376; ATE N; 1.
KW Hypothetical protein.

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SQ SEQUENCE 644 AA; 72444 MW; DDB97FC0C40C23F8 CRC64;

Query Match 67.9%; Score 53; DB 2; Length 644;
Best Local Similarity 83.3%; Pred. No. 88;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGAARASGPGGG 12
Db :||| |||||
  8 SGAASASGPGGG 19

RESULT 14
Q7QEK5 ANOGA
ID Q7QEK5 ANOGA PRELIMINARY; PRT; 1379 AA.
AC Q7QEK5;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE ENSANGP0000004747 (Fragment).
GN ORFNames=ENSANGG0000003703;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RX "The Anopheles gambiae Sequence Committee;
  RT The Anopheles gambiae re-annotation.";
  RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
  RN [2]
  RP NUCLEOTIDE SEQUENCE.
  RC STRAIN=PEST;
  RG The Anopheles gambiae Sequence Committee;
  RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
  CC -!- CAUTION: The sequence shown here is derived from an
  CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
  CC preliminary data.
  DR EMBL; AAA801008846; EAA06518.2; -; Genomic DNA.
  DR GO; GO:0016021; C:integral to membrane; IEA.
  DR GO; GO:0008305; C:integrin complex; IEA.
  DR GO; GO:0005515; F:protein binding; IEA.
  DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
  DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
  DR InterPro; IPR000413; Integrin_alpha.
  DR Pfam; PF01839; FG-GAP; 3.
  DR PRINTS; PR00357; Integrin_alpha; 1.
  DR Pfam; PR01185; INTEGRIN.
  DR SMART; SM00191; Int_alpha; 6.
  KW Cell adhesion; Integrin; Transmembrane.
  FT NON_TER 1
  SQ SEQUENCE 1379 AA; 149836 MW; 2D6945B834F3DD75 CRC64;

Query Match 67.9%; Score 53; DB 2; Length 1379;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAP 14
Db |||||
  1168 AGLRRSGPGGGPP 1181

RESULT 15
Q4NQS2 9DELTA
ID Q4NQS2 9DELTA PRELIMINARY; PRT; 924 AA.
AC Q4NQS2;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=AdenDRAFT_1169;
OS Anaeromyxobacter dehalogenans 2CP-C.

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OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
 OC Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
 OX NCBI_TaxID=290397;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=2CP-C;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Richardson P.,
 RT "Sequencing of the draft genome assembly of Anaeromyxobacter
 RT dehalogenans 2CP-C.";
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=2CP-C;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.,
 RT "Annotation of the draft genome assembly of Anaeromyxobacter
 RT dehalogenans 2CP-C.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAHD01000032; EAL77965.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 924 AA; 98272 MW; BE64DCCA32A46FA4 CRC64;

Query Match 67.3%; Score 52.5; DB 2; Length 924;
 Best Local Similarity 59.1%; Pred. No. 1.4e+02;
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QY 1 AGAARASGPG-----GGAPR 15
 DB 713 AGAARAGCGAAGVDRGGAPR 734
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 Job time : 111.882 secs

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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:14:49 ; Search time 27.8824 Seconds
(without alignments)
44.477 Million cell updates/sec

Title: US-09-529-206E-26
Perfect score: 78
Sequence: 1 AGAARASGGGGAPR 15

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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	100.0	180	1	US-08-791-495-9
2	78	100.0	180	2	US-08-937-263B-8
3	78	100.0	180	2	US-09-751-798-8
4	78	100.0	180	2	US-09-392-714-25
5	78	100.0	180	2	US-09-165-546D-15
6	78	100.0	180	2	US-09-341-829A-9
7	78	100.0	180	2	US-09-849-602-30
8	70	89.7	180	1	US-08-791-495-7
9	70	89.7	180	2	US-09-341-829A-7
10	70	89.7	210	1	US-08-791-495-5
11	70	89.7	210	2	US-09-341-829A-5
12	58	74.4	436	2	US-09-252-991A-17335
13	56	71.8	210	2	US-09-252-991A-24923
14	50	64.1	160	2	US-09-252-991A-17249
15	50	64.1	366	2	US-09-902-540-13196
16	50	64.1	421	2	US-09-252-991A-33236
17	49.5	63.5	836	2	US-09-491-356C-21
18	49	62.8	143	2	US-08-789-329C-10
19	49	62.8	172	2	US-08-789-329C-7
20	49	62.8	175	2	US-08-789-329C-3
21	49	62.8	416	2	US-09-252-991A-30219
22	48	61.5	9	2	US-09-344-040C-117
23	48	61.5	9	2	US-09-833-039A-117
24	48	61.5	136	2	US-09-252-991A-30527
25	48	61.5	329	2	US-09-252-991A-19752
26	48	61.5	370	2	US-09-252-991A-23998
27	48	61.5	809	2	US-09-252-991A-31759

28	48	61.5	1427	2	US-09-252-991A-20577	Sequence 20577, A
29	47.5	60.9	268	2	US-09-252-991A-31279	Sequence 31279, A
30	47.5	60.9	678	2	US-10-104-047-3235	Sequence 3235, Ap
31	47	60.3	134	2	US-09-252-991A-19800	Sequence 19800, A
32	47	60.3	166	2	US-09-252-991A-20512	Sequence 20512, A
33	47	60.3	214	2	US-09-852-100B-5	Sequence 5, Appli
34	47	60.3	624	2	US-09-417-197-57	Sequence 57, Appl
35	47	60.3	849	2	US-09-252-991A-21865	Sequence 21865, A
36	46	59.0	480	2	US-09-252-991A-20125	Sequence 20125, A
37	46	59.0	608	2	US-09-464-377-2	Sequence 2, Appli
38	46	59.0	608	2	US-09-464-377-3	Sequence 3, Appli
39	46	59.0	789	2	US-09-252-991A-25611	Sequence 25611, A
40	46	59.0	974	2	US-08-938-291A-4	Sequence 4, Appli
41	46	59.0	974	2	US-09-589-619-4	Sequence 4, Appli
42	45	57.7	47	1	US-08-425-069-26	Sequence 26, Appl
43	45	57.7	47	1	US-08-209-747-37	Sequence 37, Appl
44	45	57.7	47	1	US-08-458-298-37	Sequence 37, Appl
45	45	57.7	47	1	US-08-317-844B-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: IL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 78; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGAARASGGGGAPR 15
|||||
DB 48 AGAARASGGGGAPR 62

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RESULT 2
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tsang; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-937-263B-8
Query Match 100.0%; Score 78; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAPR 15
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Db 48 AGAARASGPGGGAPR 62

RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tsang; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
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; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6525177man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
;
US-09-751-798-8
Query Match 100.0%; Score 78; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAPR 15
| | | | | | | | | |
Db 48 AGAARASGPGGGAPR 62

RESULT 4
US-09-392-714-25
; Sequence 25, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tsang
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-392-714-25
Query Match 100.0%; Score 78; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAPR 15
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Db 48 AGAARASGPGGGAPR 62
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RESULT 5
US-09-165-546D-15
; Sequence 15, Application US/09165546D
; Patent No. 6723832
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
;           Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                     SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
;                     USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546D
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6723832man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15
Query Match 100.0%; Score 78; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAPR 15
Db 48 AGAARASGPGGGAPR 62

RESULT 6
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; <151> 1997-01-27

US-09-341-829A-9
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-9
Query Match 100.0%; Score 78; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAPR 15
Db 48 AGAARASGPGGGAPR 62

RESULT 7
US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Teeng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30
Query Match 100.0%; Score 78; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAPR 15
Db 48 AGAARASGPGGGAPR 62

RESULT 8
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-7

Query Match      89.7%; Score 70; DB 1; Length 180;
Best Local Similarity 93.3%; Pred. No. 0.098;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AGAARASGPGGAPR 15
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Db      48 AGAARASGPRGGAPR 62

RESULT 9
US-09-341-829A-7
; Sequence 7, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; PRIOR APPLICATION NUMBER: 1999-10-18
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-7

Query Match      89.7%; Score 70; DB 2; Length 180;
Best Local Similarity 93.3%; Pred. No. 0.098;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AGAARASGPGGAPR 15
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Db      48 AGAARASGPRGGAPR 62

RESULT 10
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

; APPLICATION NUMBER: US/08/791,495
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-5

Query Match      89.7%; Score 70; DB 1; Length 210;
Best Local Similarity 93.3%; Pred. No. 0.11;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AGAARASGPGGAPR 15
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Db      48 AGAARASGPRGGAPR 62

RESULT 11
US-09-341-829A-5
; Sequence 5, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-5

Query Match      89.7%; Score 70; DB 2; Length 210;
Best Local Similarity 93.3%; Pred. No. 0.11;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AGAARASGPGGAPR 15
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Db      48 AGAARASGPRGGAPR 62

RESULT 12
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US-09-252-991A-17335
; Sequence 17335, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17335
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17335

Query Match          74.4%; Score 58; DB 2; Length 456;
Best Local Similarity 73.3%; Pred. No. 6.8;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAPR 15
Db 277 AGAGRAAGGTGQPR 291

RESULT 13
US-09-252-991A-24923
; Sequence 24923, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24923
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24923

Query Match          71.8%; Score 56; DB 2; Length 210;
Best Local Similarity 73.3%; Pred. No. 6;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAPR 15
Db 156 AGTAAADGAGGGAPR 170

RESULT 14
US-09-252-991A-17249
; Sequence 17249, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17249
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17249

Query Match          64.1%; Score 50; DB 2; Length 160;
Best Local Similarity 69.2%; Pred. No. 26;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 AARASGPGGGAPR 15
Db 117 AGRRAGPGGSAPR 129

RESULT 15
US-09-902-540-13196
; Sequence 13196, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13196
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13196

Query Match          64.1%; Score 50; DB 2; Length 366;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAPR 15
Db 72 AGTAPAGPGATAPR 86

Search completed: March 13, 2006, 19:18:50
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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:51:56 ; Search time 90.7059 Seconds
(without alignments)
69.096 Million cell updates/sec

Title: US-09-529-206E-26

Perfect score: 78

Sequence: 1 AGAARASGPGGAPR 15

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA Main:
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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	30	4	US-10-296-734-1404
2	78	100.0	179	5	US-10-482-029-202
3	78	100.0	180	3	US-09-751-798-8
4	78	100.0	180	3	US-09-849-602-30
5	78	100.0	180	4	US-10-023-182-8
6	78	100.0	180	4	US-10-207-655-71
7	78	100.0	180	4	US-10-364-614-14
8	78	100.0	180	4	US-10-026-066-3
9	78	100.0	180	4	US-10-117-937-74
10	78	100.0	180	4	US-10-295-027-386
11	78	100.0	180	4	US-10-296-734-832
12	78	100.0	180	4	US-10-488-832-139
13	78	100.0	180	4	US-10-777-053-11
14	78	100.0	180	4	US-10-751-088-15
15	78	100.0	180	4	US-10-657-022-74
16	78	100.0	180	4	US-10-837-217-11
17	78	100.0	180	5	US-10-877-373-9
18	78	100.0	180	5	US-10-723-860-1270
19	78	100.0	180	5	US-10-871-708-7
20	78	100.0	180	5	US-10-895-523-3
21	78	100.0	180	5	US-10-182-506A-3
22	78	100.0	180	5	US-10-756-149-5024
23	78	100.0	180	6	US-11-067-064-74
24	78	100.0	180	6	US-11-067-159-74
25	78	100.0	337	3	US-09-821-883-27
26	78	100.0	397	6	US-11-144-912-27
27	78	100.0	3541	4	US-10-296-734-1454

28 70 89.7 30 4 US-10-296-734-1436 Sequence 1436, Ap
29 70 89.7 135 4 US-10-295-027-388 Sequence 388, App
30 70 89.7 135 4 US-10-188-832-141 Sequence 141, Appl
31 70 89.7 180 4 US-10-146-473-69 Sequence 69, Appl
32 70 89.7 180 4 US-10-117-937-75 Sequence 75, Appl
33 70 89.7 180 4 US-10-296-734-834 Sequence 834, Appl
34 70 89.7 180 4 US-10-468-406-4 Sequence 4, Appl
35 70 89.7 180 4 US-10-657-022-75 Sequence 75, Appl
36 70 89.7 180 5 US-10-877-373-7 Sequence 7, Appl
37 70 89.7 180 6 US-11-067-064-75 Sequence 75, Appl
38 70 89.7 180 6 US-11-067-159-75 Sequence 75, Appl
39 70 89.7 210 4 US-10-157-031-88 Sequence 88, Appl
40 70 89.7 210 4 US-10-117-937-76 Sequence 76, Appl
41 70 89.7 210 4 US-10-657-022-76 Sequence 76, Appl
42 70 89.7 210 5 US-10-877-373-5 Sequence 5, Appl
43 70 89.7 210 6 US-11-067-064-76 Sequence 76, Appl
44 70 89.7 210 6 US-11-067-159-76 Sequence 76, Appl
45 66 84.6 20 4 US-10-313-986-496 Sequence 496, App

ALIGNMENTS

RESULT 1
US-10-296-734-1404
; Sequence 1404, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1404
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA segment 4
US-10-296-734-1404

Query Match 100.0%; Score 78; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.014; 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAPR 15
DB 5 AGAARASGPGGAPR 19

RESULT 2
US-10-482-029-202
; Sequence 202, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-202

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Query Match      100.0%; Score 78; DB 5; Length 179;
Best Local Similarity 100.0%; Pred. No. 0.068; 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1 AGAARASGPGGGAPR 15
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Db 48 AGAARASGPGGGAPR 62

RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. US20020010321A1
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. US20020010321A1man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-09-751-798-8

Query Match      100.0%; Score 78; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAPR 15
   |||||
Db 48 AGAARASGPGGGAPR 62

RESULT 4
US-09-849-602-30
; Sequence 30, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
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; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-tseng
; FILE REFERENCE: L0461/7105 (JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30

Query Match      100.0%; Score 78; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGAPR 15
   |||||
Db 48 AGAARASGPGGGAPR 62

RESULT 5
US-10-023-182-8
; Sequence 8, Application US/10023182
; Publication No. US20020164665A1
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; Chen, Yao-tseng; Scanlan, Matthew;
; Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; Associated Proteins, Uses Thereof,
; Truncated Forms of NY-ESO-1, and HLA
; Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,182
; FILING DATE: 17-Dec-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/751,798
; FILING DATE: December 29, 2000
; APPLICATION NUMBER: 09/062,422
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. US20020164665A1man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-023-182-8
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Query Match      100.0%; Score 78; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGAPR 15
Db 48 AGAARASGPGGGAPR 62

RESULT 6
US-10-207-655-71
; Sequence 71, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-71

Query Match      100.0%; Score 78; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGAPR 15
Db 48 AGAARASGPGGGAPR 62

RESULT 7
US-10-364-614-14
; Sequence 14, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
; APPLICANT: JAGER, Elke
; APPLICANT: KNUTH, Alexander
; APPLICANT: OLD, Lloyd
; APPLICANT: Gnjatic, Sacha
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
; FILE REFERENCE: LUD 5726.1 CIP
; CURRENT APPLICATION NUMBER: US/10/364,614
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/355,828
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-614-14

Query Match      100.0%; Score 78; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGAPR 15
Db 48 AGAARASGPGGGAPR 62

RESULT 8
US-10-026-066-3
; Sequence 3, Application US/10026066
; Publication No. US20030215425A1
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; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
; FILE REFERENCE: CTLIMM.21CPI
; CURRENT APPLICATION NUMBER: US/10/026,066
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-026-066-3

Query Match      100.0%; Score 78; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGAPR 15
Db 48 AGAARASGPGGGAPR 62

RESULT 9
US-10-117-937-74
; Sequence 74, Application US/10117937
; Publication No. US2003020239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-74

Query Match      100.0%; Score 78; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGGAPR 15
Db 48 AGAARASGPGGGAPR 62

RESULT 10
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US-10-295-027-386
; Sequence 386, Application US/10295027
; Publication No. US2003023250A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynné, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/563,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 386
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-386

Query Match 100.0%; Score 78; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAPR 15
Db 48 AGAARASGPGGAPR 62

RESULT 11
US-10-296-734-832
; Sequence 832, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Ramshaw, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 832

; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYN501a consensus polypeptide
US-10-296-734-832

Query Match 100.0%; Score 78; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAPR 15
Db 48 AGAARASGPGGAPR 62

RESULT 12
US-10-188-832-139
; Sequence 139, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-139

Query Match 100.0%; Score 78; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAPR 15
Db 48 AGAARASGPGGAPR 62

RESULT 13
US-10-777-053-11
; Sequence 11, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: MANNK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07

;; PRIOR APPLICATION NUMBER: 60/336,968
;; PRIOR FILING DATE: 2001-11-07
;; NUMBER OF SEQ ID NOS: 979
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 11
;; LENGTH: 180
;; TYPE: PRT
;; ORGANISM: Homo sapien
US-10-777-053-11

Query Match 100.0%; Score 78; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAPR 15
Db 48 AGAARASGPGGAPR 62

RESULT 14

US-10-751-088-15
; Sequence 15, Application US/10751088
; Publication No. US20040156044A1
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; Gure, Ali, Old, Lloyd, Ritter, Geid
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
; USES THEREOF

;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: FULLBRIGHT & JAWORSKI LLP
;; STREET: 666 Fifth Avenue
;; CITY: New York City
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10158

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;; COMPUTER: IBM
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: Word

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/751,088
;; FILING DATE: 02-Jan-2004
;; CLASSIFICATION: 530

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/165,546D
;; FILING DATE: 02-Oct-1998
;; APPLICATION NUMBER: 09/062,422
;; FILING DATE: April 17, 1998
;; APPLICATION NUMBER: 08/937,263
;; FILING DATE: September 15, 1997
;; APPLICATION NUMBER: US 08/725,182
;; FILING DATE: October 3, 1996

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, Norman D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 318-3000
;; TELEFAX: (212) 318-3400

;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 180 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear

;; SEQUENCE DESCRIPTION: SEQ ID NO: 15

US-10-751-088-15

Query Match 100.0%; Score 78; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAPR 15
Db 48 AGAARASGPGGAPR 62

RESULT 15

US-10-657-022-74
; Sequence 74, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANNK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-657-022-74

Query Match 100.0%; Score 78; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAPR 15
Db 48 AGAARASGPGGAPR 62

Search completed: March 13, 2006, 20:02:26
Job time : 90.7059 secs

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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:54:06 ; Search time 10.2353 Seconds
(without alignments)
40.793 Million cell updates/sec

Title: US-09-529-206E-26

Perfect score: 78

Sequence: 1 AGAARASGPGGAPR 15

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Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB_PEP.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	78	100.0	180	7	US-11-155-288-7
2	78	100.0	240	7	US-11-021-441-28
3	66	84.6	20	6	US-10-623-155-496
4	53	67.9	306	7	US-11-096-568A-20556
5	53	67.9	353	7	US-11-096-568A-22334
6	53	67.9	358	7	US-11-096-568A-22333
7	53	67.9	420	7	US-11-096-568A-22332
8	48	61.5	359	7	US-11-096-568A-22662
9	48	61.5	391	7	US-11-096-568A-22661
10	47.5	60.9	167	7	US-11-096-568A-10542
11	47.5	60.9	678	7	US-11-072-512-3295
12	47	60.3	214	6	US-10-892-379-5
13	46	59.0	134	7	US-11-096-568A-23806
14	46	59.0	287	7	US-11-096-568A-25788
15	46	59.0	293	7	US-11-096-568A-17631
16	46	59.0	298	7	US-11-096-568A-25787
17	46	59.0	304	7	US-11-096-568A-17630
18	46	59.0	341	7	US-11-096-568A-25786
19	46	59.0	360	7	US-11-129-143-113
20	46	59.0	608	7	US-11-241-347-8
21	45	59.0	974	6	US-10-531-036-35
22	45.5	58.3	280	7	US-11-143-980-34
23	45	57.7	31	7	US-11-145-861-426
24	45	57.7	32	7	US-11-145-861-407
25	45	57.7	119	7	US-11-110-424-4

26	45	57.7	268	7	US-11-087-099-6009	Sequence 6009, Ap
27	45	57.7	413	7	US-11-096-568A-27265	Sequence 27265, A
28	45	57.7	441	7	US-11-087-099-3243	Sequence 3243, Ap
29	45	57.7	830	6	US-10-921-793-38	Sequence 38, Appl
30	45	57.7	830	6	US-10-931-198-38	Sequence 65, Appl
31	44	56.4	256	7	US-11-186-284-65	Sequence 1240, Ap
32	44	56.4	298	6	US-10-821-234-1240	Sequence 108, App
33	44	56.4	361	7	US-11-129-143-108	Sequence 107, App
34	44	56.4	368	7	US-11-129-143-107	Sequence 16, Appl
35	44	56.4	379	7	US-11-109-156-16	Sequence 2026, A
36	44	56.4	532	7	US-11-096-568A-22026	Sequence 14205, A
37	44	56.4	558	7	US-11-096-568A-26217	Sequence 14205, A
38	43	55.1	101	7	US-11-096-568A-14205	Sequence 24201, A
39	43	55.1	102	7	US-11-096-568A-24201	Sequence 8816, Ap
40	43	55.1	113	7	US-11-096-568A-8816	Sequence 14203, A
41	43	55.1	135	7	US-11-096-568A-14203	Sequence 19104, A
42	43	55.1	155	7	US-11-096-568A-19104	Sequence 318, App
43	43	55.1	280	7	US-11-052-554A-318	Sequence 19986, A
44	43	55.1	306	7	US-11-096-568A-19986	Sequence 19985, A
45	43	55.1	307	7	US-11-096-568A-19985	

ALIGNMENTS

RESULT 1
US-11-155-288-7
; Sequence 7, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J L
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNN.050A
; CURRENT APPLICATION NUMBER: US/11/155,288
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-7

Query Match 100.0%; Score 78; DB 7; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGAARASGPGGAPR 15
DB 48 AGAARASGPGGAPR 62
|||||

RESULT 2
US-11-021-441-28
; Sequence 28, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: FORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEROP
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06

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; PRIOR APPLICATION NUMBER: US 60/615,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; PRIOR FILING DATE: 2004-03-26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein
US-11-021-441-28

Query Match      100.0%; Score 78; DB 7; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGAPR 15
Db 108 AGAARASGPGGAPR 122

RESULT 3
US-10-623-155-496
; Sequence 496, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 496
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-496

Query Match      84.6%; Score 66; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAARASGPGGGA 13
Db 8 AGAARASGPGGGA 20

RESULT 4
US-11-096-568A-20556
; Sequence 20556, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20556
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; LENGTH: 306
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(306)
; OTHER INFORMATION: Ceres Seq. ID no. 12383286
US-11-096-568A-20556

Query Match      67.9%; Score 53; DB 7; Length 306;
Best Local Similarity 76.9%; Pred. No. 3.3;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GAARASGPGGAP 14
Db 89 GVARADGEGTGAP 101

RESULT 5
US-11-096-568A-22334
; Sequence 22334, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22334
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(353)
; OTHER INFORMATION: Ceres Seq. ID no. 12408544
US-11-096-568A-22334

Query Match      67.9%; Score 53; DB 7; Length 353;
Best Local Similarity 71.4%; Pred. No. 3.8;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GAARASGPGGAPR 15
Db 107 GAARGQGGGQPR 120

RESULT 6
US-11-096-568A-22333
; Sequence 22333, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22333
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(358)
; OTHER INFORMATION: Ceres Seq. ID no. 12408543
US-11-096-568A-22333

Query Match      67.9%; Score 53; DB 7; Length 358;
Best Local Similarity 71.4%; Pred. No. 3.8;
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Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GAARASGPGGAPR 15
Db 112 GAARGQGGGQPR 125

RESULT 7
US-11-096-568A-22332
; Sequence 22332, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22332
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; NAME/KEY: misc feature
; LOCATION: (1)..(420)
; OTHER INFORMATION: Ceres Seq. ID no. 12408542
US-11-096-568A-22332

Query Match 67.9%; Score 53; DB 7; Length 420;
Best Local Similarity 71.4%; Pred. No. 4.4;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GAARASGPGGAPR 15
Db 174 GAARGQGGGQPR 187

RESULT 8
US-11-096-568A-22662
; Sequence 22662, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22662
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; NAME/KEY: misc feature
; LOCATION: (1)..(359)
; OTHER INFORMATION: Ceres Seq. ID no. 12409619
US-11-096-568A-22662

Query Match 61.5%; Score 48; DB 7; Length 359;
Best Local Similarity 68.8%; Pred. No. 17;
Matches 11; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 AGAARASGPG--GGAP 14
Db 34 AGAARRAGPSAPGGAP 49

RESULT 9
US-11-096-568A-22661
; Sequence 22661, Application US/11096568A
; Publication No. US20060048240A1
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```
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22661
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; NAME/KEY: misc feature
; LOCATION: (1)..(391)
; OTHER INFORMATION: Ceres Seq. ID no. 12409618
US-11-096-568A-22661

Query Match 61.5%; Score 48; DB 7; Length 391;
Best Local Similarity 68.8%; Pred. No. 18;
Matches 11; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Qy 1 AGAARASGPG--GGAP 14
Db 66 AGAARRAGPSAPGGAP 81

RESULT 10
US-11-096-568A-10542
; Sequence 10542, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 10542
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Triticum aestivum
; NAME/KEY: misc feature
; LOCATION: (1)..(167)
; OTHER INFORMATION: Ceres Seq. ID no. 13596390
US-11-096-568A-10542

Query Match 60.9%; Score 47.5; DB 7; Length 167;
Best Local Similarity 73.3%; Pred. No. 9.9;
Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 2 GAARASGPG--GGAPR 15
Db 92 GAARGGPRGGGAPR 106

RESULT 11
US-11-072-512-3295
; Sequence 3295, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
```

APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOKYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3295
LENGTH: 678
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-3295

Query Match 60.3%; Score 47.5; DB 7; Length 678;
Best Local Similarity 48.0%; Pred. No. 34;
Matches 12; Conservative 1; Mismatches 1; Indels 11; Gaps 1;
QY 1 AGAA-----RASGGGGAP 14
|||:|||||
DB 577 AGAARPEGAKEPRPRRAAGPGGGWP 601

RESULT 12
US-10-892-379-5
Sequence 5, Application US/10892379
Publication No. US20050282999A9
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Ozenberger, Bradley A.
APPLICANT: Bard, Jonathan A.
APPLICANT: Kajkowski, Eileen M.
APPLICANT: Jacobsen, Jack S.
APPLICANT: Walker, Stephen G.
APPLICANT: Sophia, Heidi
APPLICANT: Howland, David
TITLE OF INVENTION: Beta-Amyloid Peptide-Binding Proteins and Polynucleotides
FILE REFERENCE: 31896-67300 (AHP98126P2 C1)
CURRENT APPLICATION NUMBER: US/10/892,379
CURRENT FILING DATE: 2004-07-16
PRIOR APPLICATION NUMBER: 09/852,100
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 09/774,936
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: US 09/172,990
PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: US 09/060,609
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: US 60/064,583
PRIOR FILING DATE: 1997-04-16
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 214
TYPE: PRT
ORGANISM: Homo sapiens
US-10-892-379-5

Query Match 60.3%; Score 47; DB 6; Length 214;
Best Local Similarity 69.2%; Pred. No. 14;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAARASGPGGA 13
|||:|||||
DB 47 AGAAQPEGPGGAA 59

RESULT 13
US-11-096-568A-23806
Sequence 23806, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 23806
LENGTH: 134
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(134)
OTHER INFORMATION: Ceres Seq. ID no. 12415289
US-11-096-568A-23806

Query Match 59.0%; Score 46; DB 7; Length 134;
Best Local Similarity 72.7%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 ARASGPGGGAP 14
||:|||||
DB 69 ARGAGPGGAGAP 79

RESULT 14
US-11-096-568A-25788
Sequence 25788, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 25788
LENGTH: 287
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(287)
OTHER INFORMATION: Ceres Seq. ID no. 13493532
US-11-096-568A-25788

Query Match 59.0%; Score 46; DB 7; Length 287;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AGAARASGPGGG 12
|||:|||||
DB 76 AGAAAGGPGSG 87

RESULT 15
US-11-096-568A-17631
Sequence 17631, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.

; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

; TITLE OF INVENTION: Therby

; FILE REFERENCE: 2750-1592PUS2

; CURRENT APPLICATION NUMBER: US/11/096,568A

; CURRENT FILING DATE: 2005-04-01

; NUMBER OF SEQ ID NOS: 34471

; SEQ ID NO 17631

; LENGTH: 293

; TYPE: PRT

; ORGANISM: Zea mays subsp. mays

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(293)

; OTHER INFORMATION: Ceres Seq. ID no. 12359516

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (6)..(6)

; OTHER INFORMATION: Xaa is any aa, unknown or other

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (77)..(77)

; OTHER INFORMATION: Xaa is any aa, unknown or other

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (78)..(78)

; OTHER INFORMATION: Xaa is any aa, unknown or other

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (79)..(79)

; OTHER INFORMATION: Xaa is any aa, unknown or other

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (81)..(81)

; OTHER INFORMATION: Xaa is any aa, unknown or other

; US-11-096-568A-17631

Query Match 59.0%; Score 46; DB 7; Length 293;

Best Local Similarity 75.0%; Pred. No. 25;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AGAARASGPGGG 12

Db 82 AGAAAGGPGSGG 93

Search completed: March 13, 2006, 20:03:30

Job time : 10.2353 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 18:52:59 ; Search time 105.412 Seconds
(without alignments)
58.355 Million cell updates/sec

Title: US-09-529-206E-27

Perfect score: 74

Sequence: 1 GAARASGGGGAPR 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	14	2	AAY05986 Human can
2	74	100.0	15	2	AAY05978 Human can
3	74	100.0	20	2	AAY05979 Human can
4	74	100.0	30	5	AAY05105 Human NYN
5	74	100.0	179	8	ADK68648 Epitope 1
6	74	100.0	180	2	AAY62584 Cancer as
7	74	100.0	180	2	AAY69665 Human NY-
8	74	100.0	180	2	AAY05965 Human can
9	74	100.0	180	3	AAY52430 Human tum
10	74	100.0	180	3	AAY70862 Human tum
11	74	100.0	180	3	AAB03154 Human oes
12	74	100.0	180	4	AAB69946 Human NY-
13	74	100.0	180	4	AAG67164 Amino aci
14	74	100.0	180	4	AAY01535 Human NY-
15	74	100.0	180	4	AAE07714 Human NY
16	74	100.0	180	5	AAU84818 Human NYN
17	74	100.0	180	5	AAU11543 Human tum
18	74	100.0	180	6	ABR58672 Human can
19	74	100.0	180	6	ABR48210 Human bla
20	74	100.0	180	6	ABU56508 Lung can
21	74	100.0	180	6	ABU56694 Lung can
22	74	100.0	180	6	ABP74198 Human NY-
23	74	100.0	180	6	ABU64816 Human NY-
24	74	100.0	180	6	ABR83438 Human NY-

25	74	100.0	180	7	ADC09576	Adc09576 NY-ESO-1
26	74	100.0	180	7	ADD35564	Add35564 Human NY-
27	74	100.0	180	7	ADD35568	Add35568 Human NY-
28	74	100.0	180	7	ADD25510	Add25510 Binding d
29	74	100.0	180	7	ADN39068	Adn39068 Cancer/an
30	74	100.0	180	8	ADJ54139	Adj54139 Human NY-
31	74	100.0	180	8	ADM72815	Adm72815 Human NY-
32	74	100.0	180	8	ADM73418	Adm73418 CAG-3 pro
33	74	100.0	180	8	ADM73417	Adm73417 Human NY-
34	74	100.0	180	8	ADQ18451	Adq18451 Human sof
35	74	100.0	180	8	ADQ10446	Adq10446 Autoimmun
36	74	100.0	180	8	ADS80926	Ads80926 Tumour as
37	74	100.0	180	9	ADM44353	Adm44353 Human aut
38	74	100.0	180	9	ADY85096	Ady85096 Tumour ant
39	74	100.0	180	9	ADZ28913	Adz28913 NY-ESO-1
40	74	100.0	180	9	ADZ42374	Adz42374 Immunogen
41	74	100.0	180	9	AEA35651	Aea35651 Human NY-
42	74	100.0	240	9	ADW99402	Adw99402 NY-ESO-1/
43	74	100.0	240	9	AEB80047	Aeb80047 Human NY-
44	74	100.0	397	4	AAE13122	Aae13122 NY-ESO-IC
45	74	100.0	3541	5	AAU85130	Aau85130 Human mel

ALIGNMENTS

RESULT 1

AAAY05986
ID AAY05986 standard; peptide; 14 AA.
XX
AC AAY05986;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine.
XX Homo sapiens.
XX
PN W09918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Claim 25; Page 50; 88pp; English.

CC The present sequence represents a cancer peptide that corresponds to
CC amino acid residues 49-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
CC AAY05965), a new and potent tumour antigen capable of eliciting an
CC antigen specific immune response by T cells. Cancer peptides derived from
CC CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
CC variants (see AAY05967-87), are useful as cancer vaccines that protect
CC against cancer. The invention provides: vectors and host cells (also
CC useful as vaccines); a method of diagnosis of cancer or precancer; a
CC transgenic animal; antisense oligonucleotides that inhibit expression of

CC the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
 CC cancer peptide, useful in diagnostic and detection assays; and methods
 CC for preventing or inhibiting cancer by administering a cancer peptide,
 CC with or without an HLA molecule. The cancer peptides form part of, or are
 CC derived from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
 CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
 CC treated by inducing cancer-specific T cells in vitro for subsequent
 CC return to a patient
 XX Sequence 14 AA;
 SQ

Query Match 100.0%; Score 74; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0051;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAARASGPGGAPR 14
 DB 1 GAARASGPGGAPR 14

RESULT 2
 AAY05978
 ID AAY05978 standard; peptide; 15 AA.
 XX
 AC AAY05978;

DT 16-AUG-1999 (first entry)
 DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
 XX

KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine.

XX Homo sapiens.

XX WO9918206-A2.

XX 15-APR-1999.

XX 21-SEP-1998; 98WO-US019609.

XX 08-OCT-1997; 97US-0061428P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang RF, Rosenberg SA;

XX WPI; 1999-277270/23.

XX Cancer antigen NY ESO1/CAG-3.

XX Claim 15; Page 64; 89pp; English.

CC The present sequence represents a cancer peptide that corresponds to
 CC amino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
 CC AAY05965), a new and potent tumour antigen capable of eliciting an
 CC antigen specific immune response by T cells. Cancer peptides derived from
 CC CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
 CC variants (see AAY05967-87), are useful as cancer vaccines that protect
 CC against cancer. The invention provides: vectors and host cells (also
 CC useful as vaccines); a method of diagnosis of cancer or precancer; a
 CC transgenic animal; antisense oligonucleotides that inhibit expression of
 CC the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
 CC cancer peptide, useful in diagnostic and detection assays; and methods
 CC for preventing or inhibiting cancer by administering a cancer peptide,
 CC with or without an HLA molecule. The cancer peptides form part of, or are

CC derived from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
 CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
 CC treated by inducing cancer-specific T cells in vitro for subsequent
 CC return to a patient
 XX Sequence 15 AA;
 SQ

Query Match 100.0%; Score 74; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAARASGPGGAPR 14
 DB 2 GAARASGPGGAPR 15

RESULT 3
 AAY05979
 ID AAY05979 standard; peptide; 20 AA.
 XX
 AC AAY05979;

XX 16-AUG-1999 (first entry)
 DT Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
 XX

KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine.

XX Homo sapiens.

XX Synthetic.

XX WO9918206-A2.

XX 15-APR-1999.

XX 21-SEP-1998; 98WO-US019609.

XX 08-OCT-1997; 97US-0061428P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang RF, Rosenberg SA;

XX WPI; 1999-277270/23.

XX Cancer antigen NY ESO1/CAG-3.

XX Claim 16; Page 64; 88pp; English.

CC The present sequence represents a cancer peptide that is based on amino
 CC acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965),
 CC a new and potent tumour antigen capable of eliciting an antigen specific
 CC immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-
 CC 3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-
 CC 87), are useful as cancer vaccines that protect against cancer. The
 CC invention provides: vectors and host cells (also useful as vaccines); a
 CC method of diagnosis of cancer or precancer; a transgenic animal;
 CC antisense oligonucleotides that inhibit expression of the cancer peptide
 CC or tumour antigen; antibodies reacting with a CAG-3 cancer peptide,
 CC useful in diagnostic and detection assays; and methods for preventing or
 CC inhibiting cancer by administering a cancer peptide, with or without an
 CC HLA molecule. The cancer peptides form part of, or are derived from,
 CC cancers such as primary or metastatic melanoma, thymoma, lymphoma,
 CC sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
 CC cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,

CC prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by
 CC inducing cancer-specific T cells in vitro for subsequent return to a
 CC patient

XX Sequence 20 AA;

Query Match 100.0%; Score 74; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.0071;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGPGGAPR 14
 |||||
 Db 7 GAARASGPGGAPR 20
 |||||

RESULT 4
 AAU85105
 ID AAU85105 standard; peptide; 30 AA.

XX AC AAU85105;

XX 08-MAY-2002 (first entry)

XX Human NYNSO1a segment 4.

XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
 KW viral infection; human immunodeficiency virus; melanoma;
 KW bacterial infection; Salmonella; Legionella; parasitic infection;
 KW Trypanosoma; Toxoplasma; Giardia.

OS Homo sapiens.

XX WO200190197-A1.

XX 29-NOV-2001.

XX 25-MAY-2001; 2001WO-AU000622.

XX 26-MAY-2000; 2000AU-00007761.

XX (AUSU) UNIV AUSTRALIAN NAT.

XX Thomson SA, Ramshaw IA;

XX WPI: 2002-147575/19.

XX N-PSDB; ABK36925.

XX New synthetic polypeptides having several different segments of at least
 PT one parent polypeptide linked together differently compared to the
 PT linkage in the parent polypeptide, for inducing immune response against a
 PT pathogen or cancer.

XX Example 3; Fig 27; 364pp; English.

XX The invention relates to a new synthetic polypeptide (I) comprising
 CC several different segments of at least one parent polypeptide linked
 CC together in a different relationship relative to their linkage in the
 CC parent polypeptide to impede, abrogate or otherwise alter at least one
 CC function associated with the parent polypeptide and for inducing an
 CC immune response against a pathogen or cancer. Also included are a
 CC synthetic polynucleotide encoding and a computer system for designing the
 CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
 CC are referred to as a Savine. The synthetic polypeptide is useful for
 CC modulating immune responses preferably directed against a pathogen or a
 CC cancer, (e.g., cancers of the lung, breast, ovary, kidney, bone liver,
 CC oesophagus, brain, testicle, uterus), as potentiating agents.

XX Compositions comprising the polypeptide may be used in the treatment or
 CC prophylaxis against viral (such as infections caused by HIV (human
 CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
 CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
 CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic

CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
 CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
 CC a peptide derived from a parent protein used to construct a savine of the
 CC invention

XX Sequence 30 AA;

Query Match 100.0%; Score 74; DB 5; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGPGGAPR 14
 |||||
 Db 6 GAARASGPGGAPR 19
 |||||

RESULT 5
 ADK68648
 ID ADK68648 standard; protein; 179 AA.

XX AC ADK68648;

XX 06-MAY-2004 (first entry)

XX Epitope liberation-related NV-ESO-1 protein SeqID11.

XX epitope liberation; substrate; proteasome; cytostatic; antibacterial;
 KW protozoicide; fungicide; T-cell activator; vaccine; housekeeping epitope;
 KW cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;
 KW virus; bacterium; protozoan; fungus; housekeeping proteasome system;
 KW human.

XX Homo sapiens.

XX US2003228634-A1.

XX 11-DEC-2003.

XX 07-NOV-2002; 2002US-00292413.

XX 07-NOV-2001; 2001US-0336968P.

XX (SIMA/) SIMARD J J L.

XX (DIAM/) DIAMOND D C.

XX (QIUZ/) QIU Z.

XX (LEIX/) LEI X.

XX Simard J J L, Diamond DC, Qiu Z, Lei X;

XX WPI: 2004-167209/16.

XX N-PSDB; ADK68674.

XX Identifying polypeptide suitable for epitope e.g., housekeeping epitope,
 PT liberation by contacting substrate polypeptide comprising epitope of
 PT interest, with proteasome, and assaying for liberation of epitope.

XX Example 2; SEQ ID NO 11; 67pp; English.

XX This invention relates to a novel method of identifying a polypeptide
 CC suitable for epitope liberation, including the steps of identifying an
 CC epitope of interest; providing substrate polypeptide sequence including
 CC the epitope, wherein the substrate permits processing by a proteasome;
 CC contacting the substrate with a composition including the proteasome,
 CC under conditions that support processing of the substrate by proteasome;
 CC and assaying for liberation of epitope. The invention may be useful for
 CC the development of compounds with a cytostatic, antibacterial,
 CC protozoicide or fungicide activity acting as T-cell activators. In
 CC addition, the invention may allow development of a vaccine. The invention
 CC is useful for identifying a polypeptide suitable for epitope liberation,
 CC where the epitope is a housekeeping epitope. The compositions comprising
 CC the identified housekeeping epitopes are useful in vitro in vaccine
 CC development or in the generation or expansion of cytotoxic T lymphocyte
 CC (CTL) to be used in adoptive immunotherapy. The invention is also useful

CC for activating T-cells against neoplastic cells, and cells infected with
 CC virus, bacterium, protozoan or fungus. CTL epitopes are identified based
 CC on the knowledge that such epitopes are, in fact, produced by the
 CC housekeeping proteasome system. Once identified, these epitopes, embodied
 CC as peptides, can be used to successfully immunise or induce therapeutic
 CC CTL responses against housekeeping proteasome expressing target cells in
 CC the host. The present sequence is that of a protein which is related to
 CC the method of the invention.

XX
 XX SQ Sequence 179 AA;

Query Match 100.0%; Score 74; DB 8; Length 179;
 Best Local Similarity 100.0%; Pred. No. 0.052;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAARASGPGGAPR 14
 |||||
 Db 48 GAARASGPGGAPR 61

RESULT 6
 AAW62584
 ID AAW62584 standard; protein; 180 AA.

XX AC AAW62584;

XX DT 17-SEP-1998 (first entry)

XX DE Cancer associated antigen NY-ESO-1.

XX XW Cancer associated antigen; NY-ESO-1; regression; progression; onset;
 XX XW cancer; treatment; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT FT Misc-difference 7 /note= "potential myristorylation site"

FT FT Misc-difference 9 /note= "potential myristorylation site"

FT FT Misc-difference 11 /note= "potential phosphorylation site"

FT FT Misc-difference 98 /note= "potential phosphorylation site"

FT FT Misc-difference 134 /note= "potential phosphorylation site"

FT FT Misc-difference 138 /note= "potential phosphorylation site"

XX FT WO9814464-A1.

XX PD 09-APR-1998.

XX PF 15-SEP-1997; 97WO-US016335.

XX PR 03-OCT-1996; 96US-00725182.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Chen Y, Scanlan M, Gure A, Old LJ, Jager E, Knuth A;
 PI Drijfhout JW;

XX DR WPI; 1998-286417/25.

XX DR N-PSDB; AAV38566.

XX XW New isolated cancer associated antigen - is used to develop products for
 XX the diagnosis and treatment of cancers and for monitoring cancer therapy.

XX PS Claim 8; Fig 3; 49pp; English.

XX XW The present sequence represents a cancer associated antigen. The clone
 XX from which the DNA sequence is obtained is designated NY-ESO-1. The
 XX CC specification described a method for determining regression, progression

CC of onset of a cancerous condition, comprising monitoring a sample from a
 CC patient with the cancerous condition for a parameter selected from NY-ESO
 CC -1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells
 CC specific for the peptide and an MHC molecule with which it non-covalently
 CC complexes. Methods for the treatment of a cancerous condition are also
 CC described. The NY-ESO-1 protein and peptides derived from it can be used
 CC for diagnosis and treatment of cancers and to monitor the efficacy of a
 CC therapeutic regime

XX SQ Sequence 180 AA;

Query Match 100.0%; Score 74; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.052;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAARASGPGGAPR 14
 |||||
 Db 49 GAARASGPGGAPR 62

RESULT 7
 AAW69665
 ID AAW69665 standard; protein; 180 AA.

XX AC AAW69665;

XX DT 27-OCT-1998 (first entry)

XX DE Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.

XX XW Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.

XX OS Homo sapiens.

XX PN WO9832855-A1.

XX PD 30-JUL-1998.

XX PF 27-JAN-1998; 98WO-US001445.

XX PR 27-JAN-1997; 97US-00791495.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Lethe B, Lucas S, De Smet C, Godelaine D, Boon-Falleur T;

XX DR WPI; 1998-427951/36.

XX DR N-PSDB; AAV50348.

XX PT New isolated LAGE-1 tumour associated nucleic acids - used to develop
 XX products for the diagnosis and treatment of LAGE-1 associated disorders,
 XX particularly tumours.

XX PS Example 2; Page 57-58; 73pp; English.

XX XW The present sequence represents human NY-ESO-1, formerly known as LL-1.2
 XX clone, which is used in an example from the present invention which
 XX describes LAGE-1 tumour associated protein (TAP). The present invention
 XX also describes: (1) a method for treating a subject with a disorder
 XX characterised by expression of a LAGE-1 nucleic acid molecule or an
 XX expression product, comprising administering to the subject autologous
 XX cytolytic T cells to ameliorate the disorder, where the cytolytic T cells
 XX are specific for complexes of an HLA molecule and a LAGE-1 TAP or an
 XX immunogenic fragment; (2) a method for treating a subject with a disorder
 XX characterised by expression of a LAGE-1 nucleic acid molecule or an
 XX expression product, comprising administering a LAGE-1 TAP or an
 XX immunogenic fragment to ameliorate the disorder; and (3) a method for
 XX selectively enriching a population of T cells with cytolytic T cells
 XX specific for a LAGE-1 TAP comprising contacting an isolated population of
 XX T cells with an agent presenting a complex of a LAGE TAP or an
 XX immunogenic fragment and a HLA presenting molecule to selectively enrich
 XX the isolated population of T cells with the cytolytic T cells. The
 XX methods and products from the present invention can be used for the

CC diagnosis and treatment of LAGE-1 associated disorders, particularly
 CC tumours

SQ Sequence 180 AA;

Query Match 100.0%; Score 74; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.052;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGPGGAPR 14
 |||||
 Db 49 GAARASGPGGAPR 62

RESULT 8

AAV05965
 ID AAV05965 standard; protein; 180 AA.

XX AC AAY05965;

XX XX 16-AUG-1999 (first entry)

XX DE Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.

XX KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia;
 KW non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis;
 KW melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer;
 KW breast cancer; prostate cancer; ovarian cancer; cervical cancer;
 KW bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma;
 KW tumour; diagnosis; immunotherapy; therapy; vaccine; ORF1.

XX OS Homo sapiens.

XX PN W09918206-A2. {

XX PD 15-APR-1999.

XX XX 21-SEP-1998; 98WO-US019609.

XX PR 08-OCT-1997; 97US-0061428P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Wang RF, Rosenberg SA;

XX DR WFI; 1999-277270/23.

XX DR N-PSDB; AAX58599.

XX PT Cancer antigen NY ESO1/CAG-3.

XX PS Claim 4; Fig 3A; 88pp; English.

XX CC The present sequence represents the ORF1 protein encoded by open reading
 CC frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and
 CC potent tumour antigen capable of eliciting an antigen specific immune
 CC response by T cells. Cancer peptides comprising ORF1, ORP2 (see
 CC AAY05966), portions of these peptides and their variants (see AAY05965-
 CC 87), are useful as cancer vaccines that protect the recipient from
 CC development of cancer. The invention provides: vectors and host cells
 CC (also useful as vaccines); a method of diagnosis of cancer or precancer;
 CC a transgenic animal; antisense oligonucleotides that inhibit expression
 CC of the cancer peptide or tumour antigen; antibodies reacting with the CAG
 CC -3 cancer peptide, useful in diagnostic and detection assays; and methods
 CC for preventing or inhibiting cancer by administering a cancer peptide,
 CC with or without an HLA molecule. The cancer peptides form part of, or are
 CC derived from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
 CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
 CC treated by inducing cancer-specific T cells in vitro for subsequent
 CC return to a patient

XX SQ Sequence 180 AA;

Query Match 100.0%; Score 74; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.052;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGPGGAPR 14
 |||||
 Db 49 GAARASGPGGAPR 62

RESULT 9

AAV52430

ID AAV52430 standard; protein; 180 AA.

XX AC AAY52430;

XX XX 21-OCT-2004 (revised)

DT 15-FEB-2000 (first entry)

XX XX Human tumour antigen NY-ESO-1.

XX KW Cancer; tumour; antigen; MHC; major histocompatibility complex; T-cell;
 KW cytotoxic; helper; stimulation; proliferation; treatment; diagnosis;
 KW prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;
 KW hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.

XX OS Homo sapiens.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Peptide 44..53

FT /note= "Peptide presented by MHC Class I HLA-B7"

FT Peptide 60..69

FT /note= "Peptide presented by MHC Class I HLA-B7"

FT Peptide 60..68

FT /note= "Peptide presented by MHC Class I HLA-B7"

FT Peptide 63..72

FT /note= "Peptide presented by MHC Class I HLA-B7"

FT Peptide 79..88

FT /note= "Peptide presented by MHC Class I HLA-B7"

FT Peptide 79..87

FT /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
 and HLA-B35"

FT Peptide 82..91

FT /note= "Peptide presented by MHC Class I HLA-A1"

FT Peptide 82..90

FT /note= "Peptide presented by MHC Class I HLA-A1"

FT Peptide 83..91

FT /note= "Peptide presented by MHC Class I HLA-B44"

FT Peptide 84..92

FT /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
 and HLA-B35"

FT Peptide 87..96

FT /note= "Peptide presented by MHC Class I HLA-A1"

FT Peptide 88..96

FT /note= "Peptide presented by MHC Class I HLA-B44"

FT Peptide 96..104

FT /note= "Peptide presented by MHC Class I HLA-B7"

FT Peptide 100..108

FT /note= "Peptide presented by MHC Class I HLA-B44"

FT Peptide 102..110

FT /note= "Peptide presented by MHC Class I HLA-B44"

FT Peptide 107..116

FT /note= "Peptide presented by MHC Class I HLA-A24"

FT Peptide 110..118

FT /note= "Peptide presented by MHC Class I HLA-B52"

FT Peptide 113..122

FT /note= "Peptide presented by MHC Class I HLA-B7 and HLA-B52"

FT Peptide 113..121

FT /note= "Peptide presented by MHC Class I HLA-B7"

FT Peptide 115..124

FT /note= "Peptide presented by MHC Class I HLA-A3"

FT Peptide 118. .126
FT /note= "Peptide presented by MHC Class I HLA-B35"
FT Peptide 124. .133
FT /note= "Peptide presented by MHC Class I HLA-B52"
FT Peptide 125. .133
FT /note= "Peptide presented by MHC Class I HLA-A24"
FT Peptide 138. .147
FT /note= "Peptide presented by MHC Class I HLA-B8"
FT Peptide 139. .147
FT /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 145. .153
FT /note= "Peptide presented by MHC Class I HLA-A24 and HLA-B52"
FT Peptide 153. .162
FT /note= "Peptide presented by MHC Class I HLA-B52"
FT Peptide 154. .163
FT /note= "Peptide presented by MHC Class I HLA-B52"
FT Peptide 154. .162
FT /note= "Peptide presented by MHC Class I HLA-B52"
FT Peptide 156. .167
FT /note= "Peptide (AAV52434) presented by MHC Class I HLA-A23"
FT Peptide 158. .166
FT /note= "Peptide presented by MHC Class I HLA-A3"
FT Peptide 159. .167
FT /note= "Peptide presented by MHC Class I HLA-A3"
FT Peptide 162. .170
FT /note= "Peptide presented by MHC Class I HLA-B52"
FT XX
PN W0953938-A1.
XX
XX 28-OCT-1999.
XX
XX 24-MAR-1999; 99WO-US006875.
XX
PR 17-APR-1998; 98US-00062422.
PR 02-OCT-1998; 98US-00165546.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI Gure A, Ritter G;
XX
XX WPI; 2000-038483/03.
DR N-PSDB; AAZ38380.
XX
XX Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes.
XX
XX Claim 30; Fig 3; 49pp; English.
XX
XX This sequence represents a human tumour antigen, NY-ESO-1, the cDNA
CC encoding which was isolated from an oesophagus squamous cell cancer cDNA
CC library. Tissue localisation studies revealed it to be expressed at high
CC levels in normal ovary and testis but not in normal colon, kidney, liver,
CC brain, oesophagus and skin. It was expressed in certain tumours and
CC tumour cell lines with some degree of frequency - these included melanoma
CC specimens and cell lines, and breast and bladder cancer specimens, with
CC expression in other tumour types being sporadic. Peptides derived from NY
CC -ESO-1 are bound by both MHC (major histocompatibility complex) Class I
CC and Class II molecules for presentation to T-cells. Peptides AAV52431-
CC Y52434 bind to Class I HLA-A2 molecules, thereby stimulating
CC proliferation of cytotoxic T-cells, while peptides AAV52435-Y52440 bind
CC to Class II HLA-DR53 molecules, stimulating helper T-cell proliferation.
CC The peptides derived from NY-ESO-1 may be used in methods and
CC compositions used for the treatment, diagnosis and prevention of cancers
CC (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma,
CC ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to
CC stimulate the proliferation of T cells
CC
XX Revised record issued on 21-OCT-2004 : Correction to feature table key
XX
XX Sequence 180 AA;

Query Match 100.0%; Score 74; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAARASGPGGAPR 14
| | | | | | | | | | | | | | | |
Db 49 GAARASGPGGAPR 62

RESULT 10
AAV70862
ID AAY70862 standard; protein; 180 AA.
XX
AC AAY70862;
XX
DT 31-JUL-2000 (first entry)
XX
DE Human tumour antigen, NY-ESO-1 protein.
XX
KW NY-ESO-1; CAMEL; CTL-recognised Antigen on MELanoma; human; cancer; CTL;
KW cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer;
KW melanoma; immunotherapy; immune response.
XX
OS Homo sapiens.
XX
PN W0200023584-A1.
XX
PD 27-APR-2000.
XX
PF 15-OCT-1999; 99WO-EP007832.
XX
PR 16-OCT-1998; 98EP-00119583.
XX
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (UYHO-) UNIV HOSPITAL LEIDEN.
XX
PI Schrier PI, Aarnoudse CA, Heider K, Klade C;
XX
XX WPI; 2000-339685/29.
DR N-PSDB; AAD00152.
XX
PT Tumor-associated antigen useful for cancer immunotherapy is encoded by
PT the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
XX
XX Example 3; Page 62-63; 73pp; English.
XX
XX The present sequence is the human NY-ESO-1 protein, a tumour antigen,
CC identified by screening an esophagus carcinoma cDNA library. This protein
CC is derived from open reading frame (ORF)-1 that contain epitopes of
CC tumour specific T-cells. NY-ESO-1 is expressed in different tumour types,
CC but not in healthy tissues except in testis. It also shows homology with
CC the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELanoma)
CC protein, a tumour-associated antigen. The tumour-associated antigen
CC displayed on melanoma cells is recognised by cytotoxic T lymphocytes.
CC This sequence has anticancer activity. CAMEL tumour antigen and
CC immunogenic peptides derived from it are useful for cancer immunotherapy.
CC They have the potential to induce an immune response, by eliciting a CTL
CC response. The DNA molecule is used for the construction of recombinant or
CC fusion proteins
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 74; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAARASGPGGAPR 14
| | | | | | | | | | | | | | | |
Db 49 GAARASGPGGAPR 62

RESULT 11

AAB03154
 ID AAB03154 standard; protein; 180 AA.
 AC AAB03154;
 XX
 DT 23-OCT-2000 (first entry)
 XX
 DE Human oesophageal cancer-associated antigen NY-ESO-1.
 XX
 KW Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen;
 KW oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain;
 KW antibody; diagnostic marker; drug delivery target.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Modified-site 7 Location/Qualifiers
 FT Modified-site 9 /note= "Potential N-myristoylation site"
 FT Modified-site 11 /note= "Potential N-myristoylation site"
 FT Modified-site 11 /note= "Potential N-myristoylation site"
 FT Modified-site 98 /note= "Potential O-phosphorylation site"
 FT Modified-site 134 /note= "Potential O-phosphorylation site"
 FT Modified-site 138 /note= "Potential O-phosphorylation site"
 FT Modified-site 152..172 /note= "Potential O-phosphorylation site"
 FT Domain /note= "Potential transmembrane domain"
 FT
 XX US6069233-A.
 PN
 XX 30-MAY-2000.
 PD
 XX
 XX 26-JAN-1998; 98US-00013150.
 PF
 XX 03-OCT-1996; 96US-00725381.
 PR
 XX (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (CORR) CORNELL RES FOUND INC.
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Scanlan M, Gure AO, Chen Y, Tureci O, Sahin U, Pfreundschuh M;
 PI Old LJ;
 PI
 XX WPI; 2000-410880/35.
 DR N-PSDB; AAA61483.
 XX
 XX New isolated oesophageal cancer-associated antigen useful as markers for
 PT producing antibodies and as targets for identifying abnormal conditions,
 PT e.g. infections and cancer.
 XX
 XX Example 5; Fig 3; 9pp; English.
 PS
 XX This sequence represents a human oesophageal cancer-associated antigen,
 CC NY-ESO-1. The cDNA encoding this sequence was isolated from a cDNA
 CC library prepared from a specimen of well-to-moderately differentiated
 CC squamous cell cancer of the oesophagus. Expression analysis demonstrated
 CC that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma
 CC cell lines and in normal ovary and testis tissue, but not in normal
 CC colon, kidney, liver or brain tissue. Analysis of the amino acid sequence
 CC of the protein indicates that the protein has a transmembrane domain,
 CC several N-myristoylation sites and O-phosphorylation sites and that it
 CC contains antigenic sequences in the N-terminal half of the protein. The
 CC antigen is useful as an immunogen when combined with an adjuvant, in both
 CC precursor and post- translationally modified forms, and may be used to
 CC generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic
 CC marker for oesophageal cancer, and can be utilised as a marker for the
 CC targeted delivery of therapeutic agents to oesophageal cancer cells. It
 CC can also be used to generate diagnostic or therapeutic agents
 XX
 XX Sequence 180 AA;
 SQ

Query Match 100.0%; Score 74; DB 3; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.052;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAARASGPGGGAPR 14
 |||||
 DB 49 GAARASGPGGGAPR 62
 |||||
 RESULT 12
 AAB69946
 ID AAB69946 standard; protein; 180 AA.
 XX
 AC AAB69946;
 XX
 DT 27-APR-2001 (first entry)
 XX
 DE Human NY-ESO-1 protein.
 XX
 KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
 KW HLA-A2; HLA-DR3; melanoma; adenocarcinoma; bladder carcinoma;
 KW non-small cell lung carcinoma; tumour status determination.
 XX
 OS Homo sapiens.
 XX
 PN W0200107917-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 14-JUL-2000; 2000WO-US019220.
 XX
 PR 23-JUL-1999; 99US-00359503.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (CORR) CORNELL RES FOUND INC.
 XX
 XX Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
 PI WPI; 2001-182822/18.
 DR N-PSDB; AAF58634.
 XX
 XX Method useful for determining the status (e.g. progression, regression or
 PT stability of the disease) of a cancerous condition, involves determining
 PT the levels of NY-ESO-1 specific antibodies in a sample taken from a
 PT patient.
 XX
 XX Example 5; Fig 3; 50pp; English.
 PS
 XX The present sequence is human NY-ESO-1 protein. It is provided in a
 CC specification relating to a method for determining the status of a
 CC cancerous condition in a patient with a tumour that expresses NY-ESO-1.
 CC The method comprises assaying a sample taken from the patient for
 CC antibodies that specifically bind to the NY-ESO-1 and comparing the value
 CC obtained to a prior value obtained from assay of a prior sample taken
 CC from the patient. Any difference between the values is indicative of a
 CC change in status of the cancerous condition. The method is useful for
 CC determining whether a cancerous condition is progressing, regressing or
 CC remaining stable, in particular in patients receiving treatment for a
 CC melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
 CC carcinoma
 XX
 XX Sequence 180 AA;
 SQ

Query Match 100.0%; Score 74; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.052;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAARASGPGGGAPR 14
 |||||
 DB 49 GAARASGPGGGAPR 62
 |||||

```

RESULT 13
AAG67164
ID AAG67164 standard; protein; 180 AA.
XX
XX AAG67164;
AC
DT 13-NOV-2001 (first entry)
XX
XX Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
DE
DE Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
KW HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour;
KW cancer; testis tumour.
XX
XX Homo sapiens.
OS
XX
XX WO200162917-A1.
PN
XX
XX 30-AUG-2001.
PD
XX
XX 22-JAN-2001; 2001WO-US002126.
PF
XX
XX 22-FEB-2000; 2000US-00510635.
PR
XX
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX
XX Lethe B, Boon-Falleur T;
PI
XX
XX WPI; 2001-550091/61.
DR
XX
XX N-PSDB; AAH75118.
DR
XX
XX Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful
PT for diagnosing testicular tumors.
PT
XX
XX Example 5; Fig 3; 50pp; English.
PS
XX
XX The present sequence represents cancer testis tumour antigen NY-ESO-1
CC (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at
CC least one human leukocyte antigen (HLA) binding peptide, which binds to
CC Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is
CC expressed in tumour mRNA and in testis, but not normal colon, kidney,
CC liver or brain tissue. The presence or level of expression of NY-ESO-1
CC may be assayed for the diagnosis of cancer, especially testis tumours
XX
XX Sequence 180 AA;
SQ
Query Match 100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAARASGPGGAPR 14
Db |||||
49 GAARASGPGGAPR 62

RESULT 14
AAU01535
ID AAU01535 standard; protein; 180 AA.
XX
XX AAU01535;
AC
XX
XX 18-JUL-2001 (first entry)
DT
XX
XX Human NY-ESO-1 tumour rejection antigen precursor protein.
DE
XX
XX NY-ESO-1; human; tumour rejection antigen precursor; SX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
XX
XX Homo sapiens.
OS

```

```

XX Key Location/Qualifiers
FH Modified-site 7
FT /note= "Myristoylated" 9
FT Modified-site 9
FT /note= "Myristoylated" 11
FT Modified-site 11
FT /note= "Phosphorylated" 98
FT Modified-site 134
FT /note= "Phosphorylated" 138
FT Modified-site /note= "Phosphorylated"
XX
XX WO200123560-A2.
PN
XX
XX 05-APR-2001.
PD
XX
XX 26-SEP-2000; 2000WO-US026411.
PF
XX
XX 29-SEP-1999; 99US-00408036.
PR
XX
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX
XX Tureci O, Sahin U, Pfreundschuh M;
PI
XX
XX WPI; 2001-266156/27.
DR
XX
XX N-PSDB; AAS02254.
DR
XX
XX Polypeptides binding to major histocompatibility complex class II human
PT leukocyte antigen-determining region molecule having amino acid sequence
PT found in tumor rejection antigen precursor used for stimulating
PT proliferation of helper T cells.
PT
XX
XX Claim 4; Fig 3; 62pp; English.
PS
XX
XX The sequence represents a human NY-ESO-1 tumour rejection antigen
CC precursor. NY-ESO-1 and SX-2 polypeptides, or fragments of, bind to
CC major histocompatibility complex (MHC) Class II molecules such as human
CC leukocyte antigen-determining region (HLA-DR) molecules and stimulate
CC proliferation of helper T cells. The peptides can be administered to an
CC HLA-DR positive subject in order to stimulate the helper T cells. An MHC
CC Class II HLA-DR-NY-ESO-1/SX-2 complex expressed on the surface of a cell
CC or present in free form is useful for this stimulation. The nucleic acid
CC is useful for screening for a cancerous condition, which involves
CC contacting a subject sample to a cell line transfected with the
CC immunoreactive cell (helper T cell), where interaction is indicative of
CC cancer. In addition, a sample from a patient (for example, a body fluid
CC or tissue) can be monitored for the amount of the complex present in the
CC bloodstream. This is useful for determining regression, progression or
CC onset of a cancerous condition. The method involves contacting the sample
CC with a radioactive labelled or enzyme labelled monoclonal antibody which
CC specifically binds with the complex
XX
XX Sequence 180 AA;
SQ
Query Match 100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAARASGPGGAPR 14
Db |||||
49 GAARASGPGGAPR 62

RESULT 15
AAE07714
ID AAE07714 standard; protein; 180 AA.
XX
XX AAE07714;
AC
XX
XX 06-NOV-2001 (first entry)
DT

```



```
XX Human NY ESO-1 protein.
DE
XX
XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 45..47
FT /note= "Encoded by CCCGGGGC"
XX
XX WO200155393-A2.
XX
XX 02-AUG-2001.
XX
XX 26-JAN-2001; 2001WO-US002765.
XX
XX 28-JAN-2000; 2000US-0179004P.
PR 29-SEP-2000; 2000US-0237107P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Wang R, Rosenberg SA, Zeng G;
PI
XX WPI; 2001-496851/54.
DR N-PSDB; AAD14179, AAD14180.
XX
XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis.
XX
XX Example 1; Fig 1; 134pp; English.
XX
XX The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any given
CC target antigen and/or hapten and to induce tumour-specific humoral-
CC mediated immunity against cancer. The present sequence is human NY ESO-1
CC protein
XX
XX Sequence 180 AA;
SQ
Query Match 100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. NO. 0.052;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAARASGPGGGAPR 14
Db 49 GAARASGPGGGAPR 62
Search completed: March 13, 2006, 19:03:59
Job time : 105.412 secs
```

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:04:24 ; Search time 16.6353 Seconds
(without alignments)
80.975 Million cell updates/sec

Title: US-09-529-206E-27

Perfect score: 74

Sequence: 1 GAARASGPGGGAPR 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	67.6	82	T04476	acclimation protei
2	49	66.2	222	T36115	probable oxidoredu
3	48	64.9	351	S50754	hypothetical prote
4	48	64.9	1690	T35694	ATP dependent DNA
5	45	60.8	173	AB3648	flagellar basal-bo
6	44.5	60.1	566	T21096	hypothetical prote
7	44.5	60.1	692	T21095	hypothetical prote
8	44.5	60.1	730	A36226	collagen alpha 1 c
9	44	59.5	220	E72464	hypothetical prote
10	44	59.5	269	A47008	transcription acti
11	44	59.5	286	S04673	H+-transporting tw
12	44	59.5	379	A48082	MAP kinase 3 (EC 2
13	44	59.6	900	E70894	probable infB - My
14	44	59.5	924	F87103	initiation factor
15	44	59.5	1134	A41350	adenylate cyclase
16	44	59.5	3190	T13828	CREB-binding prote
17	43	58.1	185	T36874	hypothetical prote
18	43	58.1	189	AE3136	Hypothetical prote
19	43	58.1	189	G98151	hypothetical prote
20	43	58.1	213	S42585	DNA-invertase - Rh
21	43	58.1	260	T32525	hypothetical prote
22	43	58.1	307	B72677	hypothetical prote
23	43	58.1	349	S55626	hypothetical prote
24	43	58.1	377	S28184	Ca2+/calmodulin-de
25	43	58.1	380	JC1451	Ca2+/calmodulin-de
26	43	58.1	571	I37405	polypeptide N-acet
27	43	58.1	627	T35608	polyketide hydroxy
28	43	58.1	679	S02165	regulatory protein
29	43	58.1	954	A87431	regulatory protein

30	43	58.1	1028	2	A56038	DNA-binding protei
31	43	58.1	1036	1	A34755	nitrogen regulator
32	43	58.1	1079	2	B70807	hypothetical glyci
33	43	58.1	1213	2	S16356	ovo protein - frui
34	42	56.8	143	2	H87399	peptidyl-trNA hydr
35	42	56.8	166	2	G75519	conserved hypothet
36	42	56.8	201	2	G72663	hypothetical prote
37	42	56.8	233	2	JC7618	FRAT2 protein - hu
38	42	56.8	266	1	TLB92X	tail fiber protein
39	42	56.8	327	2	T29031	hypothetical prote
40	42	56.8	333	2	C48423	homeotic protein e
41	42	56.8	335	2	S08341	myristylated alani
42	42	56.8	378	2	C87425	aldose 1-epimerase
43	42	56.8	387	2	T52451	endopeptidase Clp
44	42	56.8	435	2	T15143	hypothetical prote
45	42	56.8	436	2	T36104	conserved hypothet

ALIGNMENTS

RESULT 1

T04476

acclimation protein 2 - barley

C;Species: Hordeum vulgare (barley)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T04476

R;Phillips, J.R.; Dunn, M.A.; Hughes, M.A.

Plant Mol. Biol. 33, 1013-1023, 1997

A;Title: mRNA stability and localisation of the low temperature responsive barley gene

A;Reference number: Z15367; MUID:97299834; PMID:9154983

A;Accession: T04476

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-82 <PHI>

A;Cross-references: UNIPROT:Q40033; UNIPARC:UPI000009CE5A; EMBL:X97917; NID:G1418969; P

A;Experimental source: cv. Igri

C;Genetics:

A;Gene: btl14.2

Query Match	67.6%	Score 50;	DB 2;	Length 82;
Best Local Similarity	69.2%	Pred. No. 4.5;		
Matches	9;	Conservative	1;	Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAARASGPGGGAP 13

Db 31 GAARGAGAGGGVP 43

RESULT 2

T36115

probable oxidoreductase - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004

C;Accession: T36115

R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, April 1999

A;Reference number: Z21597

A;Accession: T36115

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-222 <MUR>

A;Cross-references: UNIPROT:Q9X887; UNIPARC:UPI00000DB008; EMBL:AL049707; PTDN:CAB41281

A;Experimental source: strain A3 (2)

C;Genetics:

A;Gene: SCOEDB:SC15.12c

C;Superfamily: NAD(P)H-dependent FMN reductase (sulfate starvation-induced protein 4);

Query Match 66.2%; Score 49; DB 2; Length 222;

Best Local Similarity 69.2%; Pred. No. 14;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAARASGPGGGAP 13

```

Db      181  GSARASGPSAGRP 193
      |:||||| | |
RESULT 3
S50754
hypothetical protein WP6 - Chlamydomonas eugametos
C:Species: Chlamydomonas eugametos
C>Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S50754
R:Woessner, J.P.; Molendijk, A.J.; van Egmond, P.; Klis, F.M.; Goodenough, U.W.; Haring,
Plant Mol. Biol. 26, 947-960, 1994
A:Title: Domain conservation in several volvocalean cell wall proteins.
A:Reference number: S50754; PMID:95093034; PMID:8000007
A:Accession: S50754
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-351 <WOE>
A:CROSS-references: UNIPROT:Q39492; UNIPARC:UPI000000A170A; EMBL:L29028; NID:G530877; PID

Query Match      64.9%; Score 48; DB 2; Length 351;
Best Local Similarity 69.2%; Pred. No. 27;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1  GAARASGPGGGAP 13
      |:||||| | |
Db      296  GSFRASPPGGPP 308

RESULT 4
T35694
ATP dependent DNA helicase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T35694
R:Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
A:Reference number: Z21587
A:Accession: T35694
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1690 <HAR>
A:CROSS-references: UNIPROT:O86821; UNIPARC:UPI000000DACB6; EMBL:AL031031; PIDN:CAAL9862.
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC7C7.16c

Query Match      64.9%; Score 48; DB 2; Length 1690;
Best Local Similarity 64.3%; Pred. No. 99;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1  GAARASGPGGGAP 14
      |:||||| | |
Db      1437  GSANGSGPGSAPR 1450

RESULT 5
AB3648
flagellar basal-body rod protein flgF [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AB3648
R:DeiVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AB3648
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-173 <KUR>
A:CROSS-references: UNIPROT:Q8YA24; UNIPARC:UPI00000058740; GB:AE008918; PIDN:AAL54349.1;
A:Experimental source: strain 16M

```

```

C:Genetics:
A:Gene: BMEI11107
A:Map position: II

Query Match      60.8%; Score 45; DB 2; Length 173;
Best Local Similarity 64.3%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1  GAARASGPGGAPR 14
      ||| ||||| |
Db      125  GAPIVLNPGGAPR 138

RESULT 6
T21096
hypothetical protein F18H3.3b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21096
R:Coles, L.
submitted to the EMBL Data Library, July 1995
A:Reference number: Z19373
A:Accession: T21096
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-566 <WIL>
A:CROSS-references: UNIPROT:Q19581; UNIPARC:UPI00000079311; EMBL:Z50110; PIDN:CAA90446.1
A:Experimental source: clone F18H3
C:Genetics:
A:Gene: CESP:F18H3.3b
A:Map position: X
A:Introns: 111/1; 215/2; 469/3; 552/3
C:Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology

Query Match      60.1%; Score 44.5; DB 2; Length 566;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY      1  GAARASGPG---GGAP 13
      ||| ||||| |
Db      534  GAPRVGGPGVQGGAP 549

RESULT 7
T21095
hypothetical protein F18H3.3a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21095
R:Coles, L.
submitted to the EMBL Data Library, July 1995
A:Reference number: Z19373
A:Accession: T21095
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-692 <WIL>
A:CROSS-references: UNIPROT:Q19579; UNIPARC:UPI00000079A30; EMBL:Z50110; PIDN:CAA90444.1
A:Experimental source: clone F18H3
C:Genetics:
A:Gene: CESP:F18H3.3a
A:Map position: X
A:Introns: 111/1; 215/2; 469/3; 552/3
C:Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology

Query Match      60.1%; Score 44.5; DB 2; Length 692;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 10; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY      1  GAARASGPG---GGAP 13
      ||| ||||| |
Db      534  GAPRVGGPGVQGGAP 549

```

RESULT 8
A36226
collagen alpha 1 chain - sea urchin (Paracentrotus lividus)
C:Species: Paracentrotus lividus (common urchin)
C>Date: 04-Oct-1991 #sequence_revision 13-Jan-1993 #text_change 09-Jul-2004
C:Accession: A36226
R/D'Alessio, M.; Ramirez, F.; Suzuki, H.R.; Solursh, M.; Gambino, R.
Proc. Natl. Acad. Sci. U.S.A. 86, 9303-9307, 1989
A:Title: Structure and developmental expression of a sea urchin fibrillar collagen gene.
A:Reference number: A36226; MUID:90083256; PMID:2594770
A:Accession: A36226
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-730 <DAA>
A:CROSS-references: UNIPROT:Q26052; UNIPARC:UPI000007B305; GB:M25282; NID:g159957; PIDN:
A:Note: the authors translated the codon CAG for residue 136 as Leu, and CAT for residue
C:Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology
C:Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix
F;523-730/Domain: fibrillar collagen carboxyl-terminal homology <FCC>

Query Match 60.1%; Score 44.5; DB 2; Length 730;
Best Local Similarity 61.1%; Pred. No. 1.4e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 5; Gaps 1;
QY 1 GAARASGPGG-----GAP 13
Db 338 GPAGSGPGGDTGSGVAP 355
||| ||||| ||||| |||||

RESULT 9
E72464
hypothetical protein APE2360 - Aeropyrum pernix (strain KI)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: E72464
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: E72464
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-220 <KAW>
A:CROSS-references: UNIPROT:Q9Y9CT; UNIPARC:UPI000005E2F9; DBJ:AP0000064; NID:g5105945;
A:Experimental source: strain KI
C:Genetics:
A:Gene: APE2360
C:Superfamily: Aeropyrum pernix hypothetical protein APE2360

Query Match 59.5%; Score 44; DB 2; Length 220;
Best Local Similarity 57.1%; Pred. No. 62;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 GAARASGPGGGAPR 14
Db 182 GATFVARPGGSDR 195
||| | : ||||| : |

RESULT 10
A47008
transcription activator NF-IL6 beta - human
N:Alternate names: d(CCAAT)-enhancer-binding protein delta, (C/EBP delta); transcription
C:Species: Homo sapiens (man)
C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A47008; A40225
R;Cleutjens, C.B.; van Bekelen, C.C.; van Dekken, H.; Smit, E.M.; Hagemeijer, A.; Wagner
Genomics 16, 520-523, 1993
A:Title: The human C/EBP delta (CRP3/CELF) gene: structure and chromosomal localization.
A:Reference number: A47008; MUID:93300531; PMID:8314590
A:Accession: A47008
A>Status: preliminary
A:Molecule type: DNA

Query Match 59.5%; Score 44; DB 2; Length 286;
Best Local Similarity 69.2%; Pred. No. 77;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 AARASGPGGGAPR 14
Db 54 ASLASGGAGAPR 66
| : ||||| |||||

RESULT 12
A48082
MAP kinase 3 (EC 2.7.1.-) - human
N:Alternate names: extracellular signal-regulated kinase 1 (ERK1); mitogen-activated pr
N:Contains: protein kinase (EC 2.7.1.37)
C:Species: Homo sapiens (man)
C>Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C:Accession: A48082; P00270; S23428; S15519; S21579
R;Charest, D.L.; Mordret, G.; Harder, K.W.; Jirik, F.; Pelech, S.L.
Mol. Cell. Biol. 13, 4679-4690, 1993
A:Title: Molecular cloning, expression, and characterization of the human mitogen-activ
A:Reference number: A48082; MUID:93330262; PMID:7687743
A:Accession: A48082
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-379 <CHA>

A:Residues: 1-269 <CLE>
A:CROSS-references: UNIPROT:P49716; UNIPARC:UPI00001274A2; GB:S63168; NID:g386449; PIDN:
A:Experimental source: prostate carcinoma cell line LNCaP
A:Note: Sequence extracted from NCBI backbone (NCBIN:134356, NCBIIP:134357)
R;Kinoehita, S.; Akira, S.; Kishimoto, T.
Proc. Natl. Acad. Sci. U.S.A. 89, 1473-1476, 1992
A:Title: A member of the C/EBP family, NF-IL6 beta, forms a heterodimer and transcripti
A:Reference number: A40225; MUID:92159071; PMID:1741402
A:Accession: A40225
A:Molecule type: DNA
A:Residues: 1, 'T', 3-12, 'G', 14-269 <KIN>
A:CROSS-references: UNIPARC:UPI0000053FFB; GB:M83667; NID:g189175; PIDN:AAA59927.1; PID
A:Note: sequence extracted from NCBI backbone (NCBIN:82662, NCBIIP:82663)
C:Genetics:
A:Gene: GDB:CEBP; CRP3; CELF
A:CROSS-references: GDB:I32661; OMIM:116898
A:Map position: 8q11-8q11
C:Superfamily: CCAAT/enhancer-binding protein alpha
C:Keywords: leucine zipper; transcription regulation
F;226-254/Region: leucine zipper motif

Query Match 59.5%; Score 44; DB 2; Length 269;
Best Local Similarity 64.3%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 GAARASGPGGGAPR 14
Db 104 GPAPLPGGPAAPR 117
||| ||||| |||||

RESULT 11
S04673
H+-transporting two-sector ATPase (EC 3.6.3.14) gamma chain - Rhodospseudomonas blastica
C:Species: Rhodospseudomonas blastica
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 31-Dec-2004
C:Accession: S04673
R;Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.
J. Mol. Biol. 179, 185-214, 1984
A:Title: Rhodospseudomonas blastica atp operon. Nucleotide sequence and transcription.
A:Reference number: S04666; MUID:85058188; PMID:6209404
A:Accession: S04673
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-286 <TYB>
A:CROSS-references: UNIPROT:P05436; UNIPARC:UPI0000126582
C:Superfamily: H(+)-transporting ATP synthase gamma chain
C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

Query Match 59.5%; Score 44; DB 2; Length 286;
Best Local Similarity 69.2%; Pred. No. 77;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 AARASGPGGGAPR 14
Db 54 ASLASGGAGAPR 66
| : ||||| |||||

RESULT 12
A48082
MAP kinase 3 (EC 2.7.1.-) - human
N:Alternate names: extracellular signal-regulated kinase 1 (ERK1); mitogen-activated pr
N:Contains: protein kinase (EC 2.7.1.37)
C:Species: Homo sapiens (man)
C>Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C:Accession: A48082; P00270; S23428; S15519; S21579
R;Charest, D.L.; Mordret, G.; Harder, K.W.; Jirik, F.; Pelech, S.L.
Mol. Cell. Biol. 13, 4679-4690, 1993
A:Title: Molecular cloning, expression, and characterization of the human mitogen-activ
A:Reference number: A48082; MUID:93330262; PMID:7687743
A:Accession: A48082
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-379 <CHA>

A;Cross-references: UNIPROT:P27361; UNIPARC:UPI0000035BE2; EMBL:X60188; NID:g31220; PIDN
A;Experimental source: hepatoma cell line HEP G2
A;Note: authors translated the codon AGC for residue 174 as Ile
F;Owaki, H.; Makar, R.; Boulton, T.G.; Cobb, M.H.; Geppert, T.D.
Biochem. Biophys. Res. Commun. 182, 1416-1422, 1992
A;Title: Extracellular signal-regulated kinases in T cells: characterization of human ER
A;Reference number: JQ1400; MUID:92171961; PMID:1540184
A;Accession: PQ0270
A;Molecule type: mRNA
A;Residues: 14-173, 'I', 175-379 <OWA>
A;Cross-references: UNIPARC:UPI000016AB99; GB:M84490; NID:g186695; PIDN:AAA36142.1; PID:
A;Experimental source: cell line CEM
R;Gonzalez, F.A.; Raden, D.L.; Rigby, M.R.; Davis, R.J.
PES Lett. 304, 170-178, 1992
A;Title: Heterogeneous expression of four MAP kinase isoforms in human tissues.
A;Reference number: S23426; MUID:92316223; PMID:1319925
A;Accession: S23428
A;Molecule type: mRNA
A;Residues: 25-173, 'I', 175-379 <GON>
A;Cross-references: UNIPARC:UPI000016A2B4; EMBL:Z11696; NID:g23882; PIDN:CAA77754.1; PID:
C;Comment: This enzyme is activated by MAP kinase (see PIR:45100 and PIR:A46723).
C;Genetics:
A;Gene: GDB:PRKM3; ERK1
A;Cross-references: GDB:135679; OMIM:601795
A;Map position: 16pter-16qter
C;Complex: monomer
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Pathway: MAP kinase cascade
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; monomer; phosphoprotein; phosphotransferase; serine/threonine-specific
F;40-330/Domain: protein kinase homology <KIN>
F;48-56/Region: protein kinase ATP-binding motif
F;202/Binding site: phosphate (Thr) (covalent) (by MAP kinase) #status predicted
F;204/Binding site: phosphate (Tyr) (covalent) (by MAP kinase) #status predicted

Query Match 59.5%; Score 44; DB 1; Length 379;
Best Local Similarity 69.2%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AARASGPGGAPR 14
||| ||| ||| |||
Db 3 AAAAQGGGGGPR 15
t

RESULT 13
B70694
probable infB - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: B70694
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70694
A;Status: preliminary
A;Molecule type: DNA
A;Title: nucleic acid sequence not shown; translation not shown
A;Residues: 1-900 <COL>
A;Cross-references: UNIPROT:P71613; UNIPARC:UPI000012D2E2; GB:Z81331; GB:AL123456; NID:9
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: infB
C;Superfamily: translation initiation factor IF-2; translation elongation factor Tu hom
C;Keywords: GTP binding; nucleotide binding; P-loop
F;399-512/Domain: translation elongation factor Tu homology <ETU>
F;405-412/Region: nucleotide-binding motif A (P-loop)
F;509-512/Region: GTP-binding NKXD motif
F;545-547/Region: GTP-binding SAK/L motif
F;411,412,432,509,510,512,545/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #

Query Match 59.5%; Score 44; DB 2; Length 900;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAARASGPGGAPR 14
||| ||| ||| |||
Db 262 GAAGAGRPGGAPR 275

RESULT 14
F87103
initiation factor IF-2 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: F87103
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: F87103
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-924 <STO>
A;Cross-references: UNIPROT:Q9Z519; UNIPARC:UPI000012D2E0; GB:AL450380; NID:g13093370; I
C;Genetics:
A;Gene: infB
C;Superfamily: translation initiation factor IF-2; translation elongation factor Tu hom

Query Match 59.5%; Score 44; DB 2; Length 924;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAARASGPGGAPR 14
||| ||| ||| |||
Db 286 GAAGAGRPGGAPR 299

RESULT 15
A41350
adenylate cyclase (EC 4.6.1.1), brain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
C;Accession: A41350
R;Krupinski, J.; Coussen, F.; Bakalyar, H.A.; Tang, W.J.; Feinstein, P.G.; Orth, K.; Sla
Science 244, 1558-1564, 1989
A;Title: Adenylate cyclase amino acid sequence: possible channel- or transporter-like str
A;Reference number: A41350; MUID:89298382; PMID:2472670
A;Accession: A41350
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1134 <KRU>
A;Cross-references: UNIPROT:P19754; UNIPARC:UPI000012886C; GB:M25579; NID:g162612; PIDN
C;Superfamily: human adenylate cyclase; guanylate cyclase catalytic domain homology
C;Keywords: phosphorus-oxygen lyase; transmembrane protein
F;248-482/Domain: guanylate cyclase catalytic domain homology <GCC>
F;819-1061/Domain: guanylate cyclase catalytic domain homology <GCC2>

Query Match 59.5%; Score 44; DB 2; Length 1134;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAARASGPGG 10
||| ||| ||| |||
Db 22 GAERAGPGG 31

Search completed: March 13, 2006, 19:16:10
Job time : 16.6353 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 18:53:23 ; Search time 101.624 Seconds
(without alignments)
97.196 Million cell updates/sec

Title: US-09-529-206E-27
Perfect score: 74
Sequence: 1 GAARASGPGGAPR 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	74	100.0	142	2	Q9NY13_HUMAN	Q9ny13 homo sapien
2	74	100.0	180	1	CTG1B_HUMAN	P78358 homo sapien
3	74	100.0	180	2	Q7LBY4_HUMAN	Q7lby4 homo sapien
4	66	89.2	210	1	CTAG2_HUMAN	O75638 homo sapien
5	54	73.0	362	2	Q63QT8_BURPS	O63qt8 burkholderi
6	54	73.0	362	2	Q62H22_BURMA	O62h22 burkholderi
7	52	70.3	321	2	Q96S27_HUMAN	Q96s27 homo sapien
8	52	70.3	447	2	Q9GRA8_GRYBI	Q9gra8 gryllus bim
9	52	70.3	644	2	Q68J75_ORYSA	O68j75 oryza sativ
10	51	68.9	337	1	CT086_HUMAN	Q9bz19 homo sapien
11	51	68.9	367	2	Q6AV33_ORYSA	O6av33 oryza sativ
12	51	68.9	559	2	Q8L680_ORYSA	O8l680 oryza sativ
13	51	68.9	867	2	Q94LD1_ORYSA	Q94ld1 oryza sativ
14	50	67.6	82	2	Q40033_HORVU	O40033 hordeum vul
15	50	67.6	111	2	Q5NTA5_CANFA	O5nta5 canis famil
16	50	67.6	194	2	Q96BU2_HUMAN	Q96bu2 homo sapien
17	50	67.6	895	2	Q4NUK4_9DELT	O4nuk4 anaeromyxob
18	50	67.6	896	2	Q96D18_HUMAN	O96d18 homo sapien
19	50	67.6	1253	2	Q6DHV6_HUMAN	O6dhv6 homo sapien
20	50	67.6	1430	2	Q9H7P9_HUMAN	Q9h7p9 homo sapien
21	49	66.2	175	1	PACA_CHICK	P41534 g glucagon-
22	49	66.2	222	2	Q9X887_STRCO	Q9x887 streptomyce
23	49	66.2	322	2	Q67FJ0_SYMTH	O67fj0 symbiobacte
24	49	66.2	327	2	Q63HT9_BURPS	O63ht9 burkholderi
25	49	66.2	330	2	Q629N3_BURMA	O629n3 burkholderi
26	49	66.2	457	2	Q7G604_ORYSA	O7g604 oryza sativ
27	49	66.2	457	2	Q94LK1_ORYSA	Q94lk1 oryza sativ
28	49	66.2	564	2	Q4NNS9_9DELT	O4nns9 anaeromyxob
29	49	66.2	589	2	Q8H3F8_ORYSA	O8h3f8 oryza sativ
30	49	66.2	695	2	Q4T320_TETNG	O4t320 tetraodon n
31	49	66.2	713	2	Q4NW70_9DELT	O4nw70 anaeromyxob

32 49 66.2 788 2 Q4QOP8_HUMAN Q4qop8 homo sapien
33 49 66.2 1379 2 Q7QEK5_ANOGA Q7qek5 anopheles g
34 48.5 65.5 924 2 Q4NQS2_9DELT Q4nqs2 anaeromyxob
35 48 64.9 88 2 Q4RDF1_TETNG Q4rdf1 tetraodon n
36 48 64.9 159 2 Q63KC9_BURPS Q63kc9 burkholderi
37 48 64.9 159 2 Q62DA7_BURMA Q62da7 burkholderi
38 48 64.9 207 2 Q8H5I9_ORYSA Q8h5i9 oryza sativ
39 48 64.9 262 2 Q5Z8E2_ORYSA Q5z8e2 oryza sativ
40 48 64.9 351 2 Q39492_CHLEU Q39492 chlamydomon
41 48 64.9 449 2 Q7FIE3_ORYSA Q7fie3 oryza sativ
42 48 64.9 487 2 Q5RL80_HUMAN Q5rl80 homo sapien
43 48 64.9 542 2 Q4UVF6_XANCP Q4uvf6 xanthomonas
44 48 64.9 558 2 Q4NUC4_9DELT Q4nuc4 anaeromyxob
45 48 64.9 717 2 Q51TX7_MAGGR Q51tx7 magnaporthe

ALIGNMENTS

RESULT 1
ID Q9NY13_HUMAN PRELIMINARY; PRT; 142 AA.
AC Q9NY13;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein LAGE-2 (Fragment).
GN Names=LAGE-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ275978; CAB76945.1; -; mRNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 142 AA; 13895 MW; 27BEE922AC4ACC7B CRC64;

Query Match 100.0%; Score 74; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 0.025; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 GAARASGPGGAPR 14
|||
DB 23 GAARASGPGGAPR 36
|||

RESULT 2
ID CTG1B_HUMAN STANDARD; PRT; 180 AA.
AC P78358;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-ESO-1).
GN Name=CTAG1B; Synonyms=CTAG, CTAG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=97203361; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
RA Chen Y.-T., Scanlan M.J., Sahin U., Tuercu O., Gure A.O., Teang S.,
Williamson B., Stockert E., Pfrendrich M., Old L.J.;
RT "A testicular antigen aberrantly expressed in human cancers detected
by autologous antibody screening.";

```

RL Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Melanoma;
RX MEDLINE=98289662; PubMed=9626360;
RA Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA de Plaen E., Boon T.;
RT "LAGE-1, a new gene with tumor specificity.";
RL Int. J. Cancer 76:903-908(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98430682; PubMed=9759882;
RA Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,
RA Schwartzentruber D.J., Rosenberg S.A.;
RT "A breast and melanoma-shared tumor antigen: T cell responses to
RT antigenic peptides translated from different open reading frames.";
RL J. Immunol. 161:3596-3606(1998).
CC -I- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide
CC variety of cancers. Detected in uterine myometrium.
CC -I- SIMILARITY: Belongs to the CTAG family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U87459; AAB49693.1; -; mRNA.
DR EMBL; AJ003149; CA005908.1; -; mRNA.
DR EMBL; AF038567; AAD05202.1; -; mRNA.
DR HGNC; HGNC:2491; CTAG1B.
DR MIM; 300156; -;
KW Antigen; Transmembrane.
FT TRANSMEM 156 172 Potential.
FT COMPIBAS 5 82 Gly-rich.
SQ SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;

Query Match 100.0%; Score 74; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAARASGPGGGAPR 14
DB 49 GAARASGPGGGAPR 62

RESULT 3
Q7LBY4 HUMAN
ID Q7LBY4 HUMAN PRELIMINARY; PRT; 180 AA.
AC Q7LBY4
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
DE antigen 1-A).
GN Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21303268;
RA "Human-mouse comparative sequence analysis of the NEMO gene reveals an
RT alternative promoter within the neighboring G6PD gene.";
RL Gene 271:93-98(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21566154; PubMed=11709543; DOI=10.1093/hmg/10.22.2557;
RA Aradhyia S., Bardaro T., Galgoczy P., Yamagata T., Resposito T.,
RA Patlan H., Ciccocioppa A., Kenwick S., Platzter M., D'Urso M.,

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RA Nelson D.L.;
RT "Multiple pathogenic and benign genomic rearrangements occur at a 35
RT kb duplication involving the NEMO and LAGE2 genes.";
RL Hum. Mol. Genet. 10:2557-2567(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Platzter M.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Platzter M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Galgoczy P., Platzter M.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99454989; PubMed=10523621;
RA De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
RT "DNA methylation is the primary silencing mechanism for a set of germ
RT line- and tumor-specific genes with a CpG-rich promoter.";
RL Mol. Cell. Biol. 19:7327-7335(1999).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF277315; AAL27014.1; -; Genomic DNA.
DR EMBL; AJ275977; CAB76943.1; -; Genomic DNA.
DR EMBL; AF277315; AAL27013.1; -; Genomic DNA.
SQ SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;

Query Match 100.0%; Score 74; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAARASGPGGGAPR 14
DB 49 GAARASGPGGGAPR 62

RESULT 4
CTAG2 HUMAN
ID CTAG2 HUMAN STANDARD; PRT; 210 AA.
AC Q75638; Q75637; Q9BU80; Q9UU89; Q9Y479;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
GN Name=CTAG2; Synonyms=ESO2, LAGE1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B).
RC TISSUE=Melanoma;
RX MEDLINE=98289662; PubMed=9626360;
RA Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA de Plaen E., Boon T.;
RT "LAGE-1, a new gene with tumor specificity.";
RL Int. J. Cancer 76:903-908(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B), AND VARIANTS
RP GLN-6; GLN-89 AND ARG-138.
RC TISSUE=Melanoma;
RX MEDLINE=99325550; PubMed=10399963;
RA Aarnoudse C.A., Van den Dool P.B., Heemskerk B., Schrier P.I.;
RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RL unexpected translation product of LAGE-1.";
RL Int. J. Cancer 82:442-448(1999).
RN [3]

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RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-1B), AND VARIANT
 ARG-138.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Kaha S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., LeWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=LAGE-1B; Synonyms=LAGE-1L;
 CC IsoId=O75638-1; Sequence=Displayed;
 CC Name=LAGE-1A; Synonyms=LAGE-1S;
 CC IsoId=O75638-2; Sequence=VSP_004301;
 CC -!- TISSUE SPECIFICITY: Testis and very low level in placenta and in
 CC some uterus samples. Observed in 25-50% of tumor samples of
 CC melanoma, non-small-cell lung carcinomas, bladder, prostate and
 CC head and neck cancers.
 CC -!- DOMAIN: A transmembrane domain is present in isoform LAGE-1A.
 CC -!- SIMILARITY: Belongs to the CTAG family.
 CC -----
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 CC EMBL; AJ223093; CAAL1117.1; -; Genomic DNA.
 CC EMBL; AJ223093; CAAL1116.1; -; Genomic DNA.
 CC EMBL; AJ223040; CAAL1043.1; -; mRNA.
 CC EMBL; AJ223041; CAAL1044.1; -; mRNA.
 CC EMBL; AJ012834; CAAL10194.1; -; mRNA.
 CC EMBL; AJ012835; CAAL10196.1; -; mRNA.
 CC EMBL; BC002833; AAH02833.1; -; mRNA.
 CC Ensembl; ENSG00000126890; Homo sapiens.
 CC HGNC; HGNC:2492; CTAG2.
 CC H-INVDB; HIX0017163; -.
 CC MIM; 300396; -.
 KW Alternative splicing; Antigen; Polymorphism; Transmembrane.
 FT COMPBIAS 5 79
 FT COMPBIAS 183 188 Poly-Pro.
 FT VARSPLIC 135 210 MSVVDQREGAGRMVVVWGLGSAPGQVARDLTPKHKV
 FT SEQRPGPPPPGAGQDGCGRGVAFNVMSAPHI -> IR
 FT LTAADHRQLQSLSSCIQLSLMLWITQCFLPVLQAPSG
 FT QRR (in isoform LAGE-1A).
 FT /FTId=VSP_004301.
 FT R -> Q.
 FT /FTId=VAR_007855.
 FT E -> Q.
 FT /FTId=VAR_007856.
 FT W -> R.
 FT /FTId=VAR_007857.
 FT SEQUENCE 210 AA; 21120 MW; 8B80E00AE55E8BE CRC64;
 Query Match 89.2%; Score 66; DB 1; Length 210;
 Best Local Similarity 92.9%; Pred. No. 0.42;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAARASGGGAPR 14
 Db |||||
 49 GAARASGGGAPR 62
 RESULT 5
 Q63QT8_BURPS
 ID Q63QT8_BURPS PRELIMINARY; PRT; 362 AA.
 AC Q63QT8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Putative DNA polymerase III.
 GN OrderedLocusNames=BPSL2936;
 OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia; pseudomallei group.
 ON NCBI_TaxID=28450;
 RX [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=K96243;
 RX PubMed=15377794; DOI=10.1073/pnas.0403302101;
 RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
 RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
 RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
 RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
 RA Chillingworth T., Cronin A., Crosssett B., Davis P., DeShazer D.,
 RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
 RA Keith K.B., Maddison M., Moule S., Price C., Quail M.A.,
 RA Rabinovitch E., Rutherford K., Sanders M., Simmonds M.,
 RA Songvilai S., Stevens K., Tumapa S., Vesaratchavest M.,
 RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
 RT "Genomic plasticity of the causative agent of melioidosis,
 Burkholderia pseudomallei.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).
 DR EMBL; BX571965; CAH36946.1; -; Genomic DNA.
 DR GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
 DR GO; GO:0006260; F:DNA replication; IEA.
 DR InterPro; IPR010372; DNA pol3 delta.
 DR InterPro; IPR005790; DNA pol3 delta.
 DR Pfam; PF06144; DNA pol3 delta; 1.
 DR TIGRFAMs; TIGR01128; hoIA; 1.
 KW Complete proteome.
 SQ SEQUENCE 362 AA; 38726 MW; D5FF3DE783D41E41 CRC64;
 Query Match 73.0%; Score 54; DB 2; Length 362;
 Best Local Similarity 83.3%; Pred. No. 28;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 ARASGGGAPR 14
 Db |||||
 348 ARASGGGAPR 359
 RESULT 6
 Q62H22_BURMA
 ID Q62H22_BURMA PRELIMINARY; PRT; 362 AA.
 AC Q62H22;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE DNA polymerase III; delta subunit (EC 2.7.7.7).
 GN Name=hoIA; OrderedLocusNames=BMA2451;
 OS Burkholderia mallei (Pseudomonas mallei).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia.
 ON NCBI_TaxID=13373;
 RX [1]
 RN NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 23344;
 RX PubMed=15377793; DOI=10.1073/pnas.0403306101;
 RA Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,

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RA  Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M., Brinkac R.J.,
RA  Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA  Durkin A.S., Gwinn M.B., Haft D.H., Khouri H.M., Kolonay J.F.,
RA  Madupu R., Mohamoud Y., Nelson W.C., Radune D., Romero C.M.,
RA  Sarria S., Sengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA  Zafar N., Zhou L., Fraser C.M.,
FT  "Structural flexibility in the Burkholderia mallei genome.";
EL  Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR  EMBL: CP000010; AAU49707.1; -; Genomic_DNA.
DR  TIGR: BNA2451; -.
DR  GO: GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR  GO: GO:0016740; F:transferase activity; IEA.
DR  GO: GO:006260; P:DNA replication; IEA.
DR  InterPro: IPR010372; DNA_pol3_delta.
DR  InterPro: IPR005790; DNA_pol3_delta.
DR  Pfam: PF06144; DNA_pol3_delta; 1.
DR  TIGRFAMs: TIGR01128; hola; 1.
KW  Complete proteome; Nucleotidyltransferase; Transferase.
SQ  SEQUENCE 362 AA; 38726 MW; D5FP3DE783D41E41 CRC64;

Query Match 73.0%; Score 54; DB 2; Length 362;
Best Local Similarity 83.3%; Pred. No. 28;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 ARASGPGGAPR 14
Db 348 ARAGPGGAPR 359
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|||||

RESULT 7
Q96S27 HUMAN
ID Q96S27_HUMAN PRELIMINARY; PRT; 321 AA.
AC Q96S27;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein gene X.
GN Name-gene X;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21096910; PubMed=11157797; DOI=10.1093/hmg/10.4.339;
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA Higgs D.R.;
RT "Sequence, structure and pathology of the fully annotated terminal 2
RT Mb of the short arm of human chromosome 16.";
RL Hum. Mol. Genet. 10:339-352(2001).
DR EMBL: AB006463; AAK61225.1; -; Genomic DNA.
DR Ensembl: ENSG0000167933; Homo sapiens.
KW Hypothetical protein.
SQ SEQUENCE 321 AA; 32979 MW; 9C8764CFA17F4CD4 CRC64;

Query Match 70.3%; Score 52; DB 2; Length 321;
Best Local Similarity 76.9%; Pred. No. 46;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ARASGPGGAPR 14
Db 5 AARAGPGGGAAR 17
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|||||

RESULT 8
Q9GRAB GRYBI
ID Q9GRAB_GRYBI PRELIMINARY; PRT; 447 AA.
AC Q9GRAB;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

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DE Hedgehog protein (Fragment).
OS Gryllus bimaculatus (Two-spotted cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999;
RN [1]_TaxID=6999;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20461145; PubMed=11003837;
RA Niwa N., Inoue Y., Nozawa A., Saito M., Misumi Y., Ohuchi H.,
RA Yoshioka H., Noji S.;
RT "Correlation of diversity of leg morphology in Gryllus bimaculatus
RT (cricket) with divergence in dpp expression pattern during leg
RT development.";
RL Development 127:4373-4381(2000).
DR EMBL: AB044709; BAB19658.1; -; mRNA.
DR HSSP: Q62226; 1VHH.
DR SMR: Q9GRA8; 49-205.
DR MEROPS: C46.001; -.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0007267; P:cell-cell signaling; IEA.
DR GO: GO:0007275; P:development; IEA.
DR GO: GO:0016539; P:intron-mediated protein splicing; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR003586; Hedgehog_and_peptidolysis; IEA.
DR InterPro: IPR003587; Hedgehog_hint_C.
DR InterPro: IPR000320; HH_signal.
DR InterPro: IPR006141; Intein_S.
DR InterPro: IPR001657; Peptidase_C46.
DR Pfam: PF01085; HH_signal; 1.
DR Pfam: PF01079; Hintt; 1.
DR PRINTS: PRO0632; SONICHHOG.
DR SMART: SM00305; HintC; 1.
DR SMART: SM00306; HintN; 1.
DR PROSITE: PS50817; INTEIN_N_TER; 1.
FT NON TER; 1
SQ SEQUENCE 447 AA; 48008 MW; 29AEFB061C3EB6F0 CRC64;

Query Match 70.3%; Score 52; DB 2; Length 447;
Best Local Similarity 78.6%; Pred. No. 63;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAARASGPGGAPR 14
Db 30 GAARACGPGRGAGR 43
|||||
|||||

RESULT 9
Q688J5 ORYZA
ID Q688J5_ORYZA PRELIMINARY; PRT; 644 AA.
AC Q688J5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein OSUNBB0012G21.2.
GN Name=OSUNBB0012G21.2;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]_TaxID=39947;
RP NUCLEOTIDE SEQUENCE.
RA Chow T.-Y., Heing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-E., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RT "Oryza sativa BAC OSUNBB0012G21 genomic sequence.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC135421; AAU10755.1; -; Genomic_DNA.

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DR Gramene; Q688J5; -.
DR GO; GO:004057; P:arginyltransferase activity; IEA.
DR GO; GO:0016598; P:protein arginylation; IEA.
DR GO; GO:0042176; P:regulation of protein catabolism; IEA.
DR InterPro; IPR007472; ATE_C.
DR InterPro; IPR007471; ATE_N.
DR Pfam; PF04377; ATE_C; 1.
DR Pfam; PF04376; ATE_N; 1.
KW Hypothetical protein.
SQ SEQUENCE 644 AA; 72444 MW; DB97FC0C40C23F8 CRC64;

Query Match 70.3%; Score 52; DB 2; Length 644;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAASGPGGG 11
| | | | | | | | | |
DB 9 GAASGPGGG 19

RESULT 10
CT086 HUMAN
ID CT086 HUMAN STANDARD; PRT; 337 AA.
AC Q9BZ19;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical protein C20orf86.
GN Name=C20orf86;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,
Beasley O.P., Bird C.P., Blake S.E., Bridgeman A.M., Brown A.J.,
Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
Lehvaselaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
Marsh V.L., Martin S.L., McConachie L.J., McInnes J.C., Nickerson T.,
Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramey H.,
Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
Whithead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- SIMILARITY: Contains 2 ANK repeats.
CC -!- SIMILARITY: Contains 1 ubiquitin-like domain.
CC -----
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DR EMBL; AL354776; CAC17565.2; -; Genomic_DNA.
DR HSP; P42771; 2A5E
DR Ensembl; ENSG00000124227; Homo sapiens.
DR HGNC; HGNC:16217; C20orf86.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00023; Ank; 2.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 2.
DR PROSITE; PSS0297; ANK REP REGION; 1.
DR PROSITE; PSS0088; ANK REPEAT; 2.
DR PROSITE; PSS0299; UBIQUITIN_1; FALSE_NEG.
DR PROSITE; PSS0053; UBIQUITIN_2; 1.
KW ANK repeat; Hypothetical protein; Polymorphism; Repeat.
FT DOMAIN 88 164 Ubiquitin-like.
FT REPEAT 211 241 ANK 1.
FT REPEAT 244 273 ANK 2.
FT VARIANT 287 287 R -> C (in dbSNP:584855).
FT /FTID=VAR_014400.
SQ SEQUENCE 337 AA; 36714 MW; EC8BA4AD414756CB CRC64;

Query Match 68.9%; Score 51; DB 1; Length 337;
Best Local Similarity 71.4%; Pred. No. 66;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAASGPGGGAPR 14
| | | | | | | | | |
DB 9 GAASGPGGGASR 22

RESULT 11
Q6AV33 ORYZA
ID Q6AV33 ORYZA PRELIMINARY; PRT; 367 AA.
AC Q6AV33;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein OSUNBa0063J18.9.
GN Name=OSUNBa0063J18.9;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
Padrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSUNBa0063J18 genomic sequence.";
RN Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC107206; AAT77052.1; -; Genomic_DNA.
DR Gramene; Q6AV33; -.
KW Hypothetical protein.
SQ SEQUENCE 367 AA; 37474 MW; B8C62D9D4CC18C86 CRC64;

Query Match 68.9%; Score 51; DB 2; Length 367;
Best Local Similarity 76.9%; Pred. No. 71;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 AARASGPGGGAPR 14
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DB 91 AARASGPGGGASR 103

RESULT 12

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RA Uterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
RA White O., Fraser C.M.;
RA Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RA Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC084404; AAK50601.1; -; Genomic_DNA.
DR Gramene; Q94LD1; -.
DR InterPro; IPR007228; DUF390.
DR InterPro; IPR007321; Transposase_28.
DR Pfam; PF04094; DUF390; 3.
DR Pfam; PF04195; Transposase_28; 1.
KW Hypothetical protein.
SQ SEQUENCE 867 AA; 92812 MW; 7365009715EDDC21 CRC64;

Query Match 68.9%; Score 51; DB 2; Length 867;
Best Local Similarity 64.3%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAARASGPGGGAPR 14
| : || |||||
DB 206 GGSRAGPGGGGR 219

RESULT 14
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ID Q40033_HORVU PRELIMINARY; PRT; 82 AA.
AC Q40033;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE BLT14.2 protein.
GN Name=blt14.2;
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97299834; PubMed=9154983; DOI=10.1023/A:1005717613224;
RA Phillips J.R., Dunn M.A., Hughes M.A.;
RT "RNA stability and localisation of the low temperature responsive
RT barley gene family blt14."
RL Plant Mol. Biol. 33:1013-1023 (1997).
DR EMBL; X97917; CAA66490.1; -; Genomic_DNA.
DR FIR; T04476; T04476.
SQ SEQUENCE 82 AA; 7752 MW; FA952DCA3CD640A7 CRC64;

Query Match 67.6%; Score 50; DB 2; Length 82;
Best Local Similarity 69.2%; Pred. No. 24;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAARASGPGGGAP 13
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DB 31 GAARGAGGGGVP 43

RESULT 15
Q5NTA5_CANPA
ID Q5NTA5_CANPA PRELIMINARY; PRT; 111 AA.
AC Q5NTA5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Pancreatic duodenal homeobox gene 1 (Fragment).
GN Name=PDX-1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;

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RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Takagi K., Neo S., Furuichi M., Watanabe M., Kaneaku N., Hisasue M.,
RA Teuchiya R., Yamada T.,
RT "Canine pdx-1.",
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB196439; BAD77930.1; -; mRNA.
DR GO; GO:0005634; C:nucleus; IEA.
KW Nuclear protein.
FT NON_TER 1
FT NON_TER 111
SQ SEQUENCE 111 AA; 11740 MW; 4565A9E88EDEC91E CRC64;

Query Match      67.6%; Score 50; DB 2; Length 111;
Best Local Similarity 64.3%; Pred. No. 32;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAARASGFGGAPR 14
Db 15 GGSRRASSFGGAQPR 28

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Search completed: March 13, 2006, 19:14:27
Job time : 102.624 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:14:49 ; Search time 26.0235 Seconds
(without alignments)
44.477 Million cell updates/sec

Title: US-09-529-206E-27

Perfect score: 74

Sequence: 1 GAARASGPGGAPR 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
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4: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	180	1	US-08-791-495-9
2	74	100.0	180	2	US-08-937-263B-8
3	74	100.0	180	2	US-09-751-798-8
4	74	100.0	180	2	US-09-392-714-25
5	74	100.0	180	2	US-09-165-546D-15
6	74	100.0	180	2	US-09-341-829A-9
7	74	100.0	180	2	US-09-849-602-30
8	66	89.2	180	1	US-08-791-495-7
9	66	89.2	180	2	US-09-341-829A-7
10	66	89.2	210	1	US-08-791-495-5
11	66	89.2	210	2	US-09-341-829A-5
12	54	73.0	456	2	US-09-352-991A-17335
13	52	70.3	210	2	US-09-352-991A-24923
14	50	67.6	160	2	US-09-252-991A-17249
15	49	66.2	143	2	US-08-789-329C-10
16	49	66.2	172	2	US-08-789-329C-7
17	49	66.2	175	2	US-08-789-329C-3
18	49	66.2	416	2	US-09-352-991A-30219
19	48	64.9	9	2	US-09-344-040C-117
20	48	64.9	9	2	US-09-833-039A-117
21	48	64.9	196	2	US-09-352-991A-30527
22	48	64.9	329	2	US-09-352-991A-19752
23	48	64.9	421	2	US-09-352-991A-32326
24	48	64.9	803	2	US-09-352-991A-31759
25	48	64.9	1427	2	US-09-352-991A-20577
26	47.5	64.2	268	2	US-09-352-991A-31279
27	47	63.5	370	2	US-09-352-991A-23998

28 46.5 62.8 678 2 US-10-104-047-3295 Sequence 3295, Ap
29 46 62.2 366 2 US-09-902-540-13196 Sequence 13196, A
30 46 62.2 799 2 US-09-252-991A-25611 Sequence 25611, A
31 45.5 61.5 836 2 US-09-491-356C-21 Sequence 21, Appl
32 45 60.8 134 2 US-09-252-991A-26710 Sequence 26710, A
33 45 60.8 187 2 US-09-252-991A-29442 Sequence 29442, A
34 45 60.8 191 2 US-09-252-991A-23951 Sequence 23951, A
35 45 60.8 262 2 US-09-252-991A-19030 Sequence 19030, A
36 45 60.8 321 1 US-08-362-670B-26 Sequence 26, Appl
37 45 60.8 321 2 US-08-333-576C-26 Sequence 26, Appl
38 45 60.8 321 2 US-08-808-324-26 Sequence 26, Appl
39 45 60.8 321 2 US-09-945-182-26 Sequence 26, Appl
40 45 60.8 321 4 PCT-US94-14030A-26 Sequence 26, Appl
41 45 60.8 679 2 US-09-352-991A-27111 Sequence 27111, A
42 45 60.8 727 2 US-09-302-540-12383 Sequence 12383, A
43 45 60.8 950 2 US-09-252-991A-25927 Sequence 25927, A
44 44 59.5 186 2 US-09-252-991A-16943 Sequence 16943, A
45 44 59.5 242 2 US-08-220-602B-23 Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-495-9

Query Match 100.0%; Score 74; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.025; 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;
QY 1 GAARASGPGGAPR 14
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Db 49 GAARASGPGGAPR 62

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RESULT 2
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tsang; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-08-937-263B-8

Query Match 100.0%; Score 74; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAARASGPGGGAPR 14
Db 49 GAARASGPGGGAPR 62

RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
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; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6525177man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-09-751-798-8

Query Match 100.0%; Score 74; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAARASGPGGGAPR 14
Db 49 GAARASGPGGGAPR 62

RESULT 4
US-09-392-714-25
; Sequence 25, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tsang
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 180
; TYPE: PPT
; ORGANISM: Homo sapiens
US-09-392-714-25

Query Match 100.0%; Score 74; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAARASGPGGGAPR 14
Db 49 GAARASGPGGGAPR 62
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RESULT 5
US-09-165-546D-15
; Sequence 15, Application US/09165546D
; Patent No. 6723832
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
; USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546D
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6723832man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15

Query Match 100.0%; Score 74; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGPGGGAPR 14
| | | | | | | | | | | | | | | |
Db 49 GAARASGPGGGAPR 62

RESULT 6
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; <151> 1997-01-27

; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-9

Query Match 100.0%; Score 74; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGPGGGAPR 14
| | | | | | | | | | | | | | | |
Db 49 GAARASGPGGGAPR 62

RESULT 7
US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30

Query Match 100.0%; Score 74; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGPGGGAPR 14
| | | | | | | | | | | | | | | |
Db 49 GAARASGPGGGAPR 62

RESULT 8
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-7

Query Match      89.2%; Score 66; DB 1; Length 180;
Best Local Similarity 92.9%; Pred. No. 0.25;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAARASGPGGGAPR 14
      ||||| |||||
Db      49 GAARASGPRGGAPR 62

RESULT 9
US-09-341-829A-7
; Sequence 7, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-7

Query Match      89.2%; Score 66; DB 2; Length 180;
Best Local Similarity 92.9%; Pred. No. 0.25;
Matches 13; Conservative 0; Mismatches 0; Gaps 0;

QY      1 GAARASGPGGGAPR 14
      ||||| |||||
Db      49 GAARASGPRGGAPR 62

RESULT 10
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-5

Query Match      89.2%; Score 66; DB 1; Length 210;
Best Local Similarity 92.9%; Pred. No. 0.28;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAARASGPGGGAPR 14
      ||||| |||||
Db      49 GAARASGPRGGAPR 62

RESULT 11
US-09-341-829A-5
; Sequence 5, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-5

Query Match      89.2%; Score 66; DB 2; Length 210;
Best Local Similarity 92.9%; Pred. No. 0.28;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAARASGPGGGAPR 14
      ||||| |||||
Db      49 GAARASGPRGGAPR 62

RESULT 12

```

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US-09-252-991A-17335
; Sequence 17335, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17335
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17335

Query Match 73.0%; Score 54; DB 2; Length 456;
Best Local Similarity 71.4%; Pred. No. 18;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAARASGPGGGAPR 14
   |||:|||||
Db 278 GAGRAAGPGTGQPR 291
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RESULT 13
US-09-252-991A-24923
; Sequence 24923, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24923
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24923

Query Match 70.3%; Score 52; DB 2; Length 210;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAARASGPGGGAPR 14
   |||:|||||
Db 157 GTAAADGAGGGAPR 170
   |||:|||||

RESULT 14
US-09-252-991A-17249
; Sequence 17249, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17249
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17249

Query Match 67.6%; Score 50; DB 2; Length 160;
Best Local Similarity 69.2%; Pred. No. 22;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 AARASGPGGGAPR 14
   |||:|||||
Db 117 AGRAGPGGSAPR 129
   |||:|||||

RESULT 15
US-08-789-329C-10
; Sequence 10, Application US/08789329C
; Patent No. 6165755
; GENERAL INFORMATION:
; APPLICANT: SHERWOOD ET AL.
; TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL
; TITLE OF INVENTION: FOR IMPROVED POULTRY PRODUCTION
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204-2988
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: WordPerfect 7.0 & ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,329C
; FILING DATE: 01/23/97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Earp, David J.
; REGISTRATION NUMBER: 41,401
; REFERENCE/DOCKET NUMBER: 2847-46468/DJE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 143 aa
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-789-329C-10

Query Match 66.2%; Score 49; DB 2; Length 143;
Best Local Similarity 69.2%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AARASGPGGGAPR 14
   |||:|||||
Db 54 ALRAGAPGGGPR 66
   |||:|||||
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Search completed: March 13, 2006, 19:18:51
Job time : 27.0235 secs

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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:51:56 ; Search time 84.6588 Seconds
(without alignments)
69.096 Million cell updates/sec

Title: US-09-529-206E-27

Perfect score: 74

Sequence: 1 GAARASGGGGAPR 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA_Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	30	4	US-10-296-734-1404
2	74	100.0	179	5	US-10-482-029-202
3	74	100.0	180	3	US-09-751-798-8
4	74	100.0	180	3	US-09-849-602-30
5	74	100.0	180	4	US-10-023-182-8
6	74	100.0	180	4	US-10-207-655-71
7	74	100.0	180	4	US-10-364-614-14
8	74	100.0	180	4	US-10-026-066-3
9	74	100.0	180	4	US-10-117-937-74
10	74	100.0	180	4	US-10-295-027-386
11	74	100.0	180	4	US-10-296-734-832
12	74	100.0	180	4	US-10-188-832-139
13	74	100.0	180	4	US-10-777-053-11
14	74	100.0	180	4	US-10-751-088-15
15	74	100.0	180	4	US-10-657-022-74
16	74	100.0	180	4	US-10-837-217-11
17	74	100.0	180	5	US-10-877-373-9
18	74	100.0	180	5	US-10-723-860-1270
19	74	100.0	180	5	US-10-871-708-7
20	74	100.0	180	5	US-10-895-523-3
21	74	100.0	180	5	US-10-182-506A-3
22	74	100.0	180	5	US-10-756-149-5024
23	74	100.0	180	6	US-11-067-064-74
24	74	100.0	180	6	US-11-067-159-74
25	74	100.0	397	3	US-09-821-883-27
26	74	100.0	397	4	US-11-144-912-27
27	74	100.0	3541	4	US-10-296-734-1454

28	66	89.2	30	4	US-10-296-734-1436	Sequence 1436, Ap
29	66	89.2	135	4	US-10-295-027-388	Sequence 388, App
30	66	89.2	135	4	US-10-188-832-141	Sequence 141, App
31	66	89.2	180	4	US-10-146-473-69	Sequence 69, Appl
32	66	89.2	180	4	US-10-117-937-75	Sequence 75, Appl
33	66	89.2	180	4	US-10-296-734-834	Sequence 834, App
34	66	89.2	180	4	US-10-468-406-4	Sequence 4, Appli
35	66	89.2	180	4	US-10-657-022-75	Sequence 75, Appl
36	66	89.2	180	5	US-10-877-373-7	Sequence 7, Appli
37	66	89.2	180	6	US-11-067-064-75	Sequence 75, Appl
38	66	89.2	180	6	US-11-067-159-75	Sequence 75, Appl
39	66	89.2	210	4	US-10-157-031-88	Sequence 88, Appl
40	66	89.2	210	4	US-10-117-937-76	Sequence 76, Appl
41	66	89.2	210	5	US-10-657-022-76	Sequence 76, Appl
42	66	89.2	210	5	US-10-877-373-5	Sequence 5, Appli
43	66	89.2	210	6	US-11-067-064-76	Sequence 76, Appl
44	66	89.2	210	6	US-11-067-159-76	Sequence 76, Appl
45	62	83.8	20	4	US-10-313-986-496	Sequence 496, App

ALIGNMENTS

RESULT 1
US-10-296-734-1404
; Sequence 1404, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1404
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA segment 4
US-10-296-734-1404

Query Match 100.0%; Score 74; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGGGGAPR 14
Db 6 GAARASGGGGAPR 19

RESULT 2
US-10-482-029-202
; Sequence 202, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-202

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Query Match      100.0%; Score 74; DB 5; Length 179;
Best Local Similarity 100.0%; Pred. No. 0.14; 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY      1 GAARASGPGGGAPR 14
      |||||
Db      49 GAARASGPGGGAPR 62
      |||||

RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. US20020010321A1
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. US20020010321A1man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-09-751-798-8

Query Match      100.0%; Score 74; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.14; 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY      1 GAARASGPGGGAPR 14
      |||||
Db      49 GAARASGPGGGAPR 62
      |||||

RESULT 4
US-09-849-602-30
; Sequence 30, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
```

```
Query Match      100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAARASGPGGGAPR 14
   |||||
Db 49 GAARASGPGGGAPR 62

RESULT 6
US-10-207-655-71
; Sequence 71, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-71

Query Match      100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAARASGPGGGAPR 14
   |||||
Db 49 GAARASGPGGGAPR 62

RESULT 7
US-10-364-614-14
; Sequence 14, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
; APPLICANT: JAGER, Elke
; APPLICANT: KNUTH, Alexander
; APPLICANT: OLD, Lloyd
; APPLICANT: Grnjatic, Sacha
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
; FILE REFERENCE: LUD 5726.1 CIP
; CURRENT APPLICATION NUMBER: US/10/364,614
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/355,828
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-614-14

Query Match      100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAARASGPGGGAPR 14
   |||||
Db 49 GAARASGPGGGAPR 62

RESULT 8
US-10-026-066-3
; Sequence 3, Application US/10026066
; Publication No. US20030215425A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
; TITLE OF INVENTION: PRESENTING CELLS
; FILE REFERENCE: CTLLM.21C1C
; CURRENT APPLICATION NUMBER: US/10/026,066
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-026-066-3

Query Match      100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAARASGPGGGAPR 14
   |||||
Db 49 GAARASGPGGGAPR 62
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```
RESULT 9
US-10-117-937-74
; Sequence 74, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLLM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-74

Query Match      100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAARASGPGGGAPR 14
   |||||
Db 49 GAARASGPGGGAPR 62

RESULT 10
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US-10-295-027-386
; Sequence 386, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natesha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 019501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 386
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-386

```

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Query Match      100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GAARASGPGGAPR 14
|||
Db 49 GAARASGPGGAPR 62

```

RESULT 11
US-10-296-734-832
; Sequence 832, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 832

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;
; LENGTH: 180
; TYPE: PRMT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYNsola consensus polypeptide
US-10-296-734-832

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Query Match      100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Caps 0;
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Qy 1 GAARASPGGGAPR 14
|||
Db 49 GAARASPGGGAPR 62

RESULT 12

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US-10-188-832-139
; Sequence 139, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-139

```

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Query Match      100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GAARASGPGGAPR 14
|||
Db 49 GAARASGPGGAPR 62

RESULT 13

```

US-10-777-053-11
; Sequence 11, Application US/10777053
; Publication No. US2004013208A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TARGET OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MAN/K.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07

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; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-777-053-11

Query Match 100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGPGGAPR 14
Db 49 GAARASGPGGAPR 62

RESULT 14

US-10-751-088-15
; Sequence 15, Application US/10751088
; Publication No. US2004015804A1
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
; USES THEREOF

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10158
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/751,088
FILING DATE: 02-Jan-2004
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546D
FILING DATE: 02-Oct-1998
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
APPLICATION NUMBER: US 08/725,182
FILING DATE: October 3, 1996

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 318-3400

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 180 amino acids
TYPE: amino acid
TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-10-751-088-15

Query Match 100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGPGGAPR 14
Db 49 GAARASGPGGAPR 62

RESULT 15

US-10-657-022-74
; Sequence 74, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANNK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-657-022-74

Query Match 100.0%; Score 74; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAARASGPGGAPR 14
Db 49 GAARASGPGGAPR 62

Search completed: March 13, 2006, 20:02:27
Job time : 85.6588 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:54:06 ; Search time 9.55294 Seconds
(without alignments)
40.793 Million cell updates/sec

Title: US-09-529-206E-27

Perfect score: 74

Sequence: 1 GAARASGPGGAPR 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 161657 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	180	7	US-11-155-288-7
2	74	100.0	240	7	US-11-021-441-28
3	62	83.8	20	6	US-10-623-155-496
4	53	71.6	306	7	US-11-096-568A-20556
5	53	71.6	353	7	US-11-096-568A-22334
6	53	71.6	358	7	US-11-096-568A-22332
7	53	71.6	420	7	US-11-096-568A-22332
8	47.5	64.2	167	7	US-11-096-568A-10542
9	46.5	62.8	678	7	US-11-072-512-3295
10	46	62.2	134	7	US-11-096-568A-23806
11	45.5	61.5	280	7	US-11-143-980-34
12	45	60.8	413	7	US-11-096-568A-27265
13	45	60.8	830	6	US-10-921-793-38
14	45	60.8	830	6	US-10-931-198-38
15	44	59.5	298	6	US-10-821-234-1240
16	44	59.5	328	7	US-11-096-568A-22662
17	44	59.5	361	7	US-11-129-143-108
18	44	59.5	368	7	US-11-129-143-107
19	44	59.5	379	7	US-11-109-156-16
20	44	59.5	391	7	US-11-096-568A-22661
21	44	59.5	558	7	US-11-096-568A-28217
22	44	59.5	974	6	US-10-531-036-35
23	43	58.1	113	7	US-11-096-568A-8816
24	43	58.1	155	7	US-11-096-568A-19104
25	43	58.1	214	6	US-10-892-379-5

26	43	58.1	306	7	US-11-096-568A-19986	Sequence 19986, A
27	43	58.1	307	7	US-11-096-568A-19985	Sequence 19985, A
28	43	58.1	314	7	US-11-096-568A-19984	Sequence 19984, A
29	43	58.1	1079	7	US-11-052-554A-145	Sequence 145, App
30	42	56.8	162	7	US-11-096-568A-641	Sequence 641, App
31	42	56.8	169	7	US-11-096-568A-12208	Sequence 12208, A
32	42	56.8	189	7	US-11-107-029-4	Sequence 4, Appli
33	42	56.8	249	7	US-11-096-568A-23045	Sequence 23045, A
34	42	56.8	287	7	US-11-096-568A-25788	Sequence 25788, A
35	42	56.8	293	7	US-11-096-568A-17631	Sequence 17631, A
36	42	56.8	296	7	US-11-096-568A-21195	Sequence 21195, A
37	42	56.8	298	7	US-11-096-568A-25787	Sequence 25787, A
38	42	56.8	304	7	US-11-096-568A-17630	Sequence 17630, A
39	42	56.8	333	7	US-11-096-568A-21193	Sequence 21193, A
40	42	56.8	341	7	US-11-096-568A-25786	Sequence 25786, A
41	42	56.8	360	7	US-11-129-143-113	Sequence 113, App
42	42	56.8	374	7	US-11-129-143-112	Sequence 112, App
43	42	56.8	608	7	US-11-241-347-8	Sequence 8, Appli
44	42	56.8	625	7	US-11-143-984A-39	Sequence 39, Appl
45	42	56.8	625	7	US-11-143-984A-110	Sequence 110, App

ALIGNMENTS

RESULT 1

US-11-155-288-7
; Sequence 7, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J L
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; FILE REFERENCE: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; CURRENT FILING DATE: 2005-06-17
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-7

Query Match 100.0%; Score 74; DB 7; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAARASGPGGAPR 14
DB 49 GAARASGPGGAPR 62

RESULT 2

US-11-021-441-28
; Sequence 28, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; FILE REFERENCE: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; CURRENT FILING DATE: 2004-12-23
; PRIOR FILING DATE: 2004-10-06

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, PRIOR APPLICATION NUMBER: US 60/615,287
, PRIOR FILING DATE: 2004-10-01
, PRIOR APPLICATION NUMBER: US 60/599,377
, PRIOR FILING DATE: 2004-08-05
, PRIOR APPLICATION NUMBER: PCT/US2004/23881
, PRIOR FILING DATE: 2004-07-23
, PRIOR APPLICATION NUMBER: US 10/893,599
, PRIOR FILING DATE: 2004-06-30
, PRIOR APPLICATION NUMBER: US 60/556,744
, PRIOR FILING DATE: 2004-03-26
, NUMBER OF SEQ ID NOS: 129
, SOFTWARE: Fast-Seq for Windows Version 4.0
, SEQ ID NO 28
, LENGTH: 240
, TYPE: PRT
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: Fusion protein
US-11-021-441-28

```

```

Query Match      100.0%; Score 74; DB 7; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 14; Conservative 0; Mismatches 0; Indels

Qy 1 GAARASGPGGGAPR 14
    |||||
Db 109 GAARASGPGGGAPR 122
    |||||

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```

RESULT 3
JS-10-623-155-496      '
; Sequence 496, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Ranger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND
; TITLE OF INVENTION: AND DIAGNOSIS O
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/62
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version
; SEQ ID NO 496
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-496

```

```

Query Match      83.8%; Score 62; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 12; Conservative 0; Mismatches 0; Indels
Qy      1 GAARASGPGGGA 12
        | | | | | | | |
Db      9 GAARASGPGGGA 20

```

```

RESULT 4
; US-11-096-568A-20556
; Sequence 20556, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Theryb
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20556

```

```

; LENGTH: 306
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(306)
; OTHER INFORMATION: Ceres Seq. ID no. 12383286
US-11-096-568A-20556

```

Query Match	71.6%;	Score 53;	DB 7;	Length 306;
Best Local Similarity	76.9%;			
Pred. No. 2.7;				
Matches 10;	Conservative	0;	Mismatches	3; Indels
Qy	1	GAARASGPGGGAP	13	
Db	89	GVARADGPGTTGAP	101	

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RESULT 5
US-11-096-568A-22334
; Sequence 22334, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22334
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(353)
; OTHER INFORMATION: Ceres Seq. ID no. 12408544
US-11-096-568A-22334

```

```

Query Match          71.6%;   Score 53;   DB 7;   Length 353;
Best Local Similarity 71.4%;   Pred. No. 3.1;
Matches 10;   Conservative 0;   Mismatches 4;   Indels 0;   Gaps 0
Qy      1  GAARASGPGGGAPR 14
          |||||  |||||  ||
Db      107 GAARGGPGGGEQPR 120

```

```

RESULT 6
US-11-096-568A-22333
; Sequence 22333, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22333
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(358)
; OTHER INFORMATION: Ceres Seq. ID no. 12408543
US-11-096-568A-22333

Query Match          71.6%;   Score 53;   DB 7;   Length 358;
Best Local Similarity 71.4%;   Pred. No. 3.1;

```

```

Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAARASGPGGAPR 14
Db 112 GAARGQPGGEQPR 125

RESULT 7
US-11-096-568A-22332
; Sequence 22332, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22332
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(420)
; OTHER INFORMATION: Ceres Seq. ID no. 12408542
US-11-096-568A-22332

Query Match 71.6%; Score 53; DB 7; Length 420;
Best Local Similarity 71.4%; Pred. No. 3.6;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAARASGPGGAPR 14
Db 174 GAARGQPGGEQPR 187

RESULT 8
US-11-096-568A-10542
; Sequence 10542, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 10542
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(167)
; OTHER INFORMATION: Ceres Seq. ID no. 13596390
US-11-096-568A-10542

Query Match 64.2%; Score 47.5; DB 7; Length 167;
Best Local Similarity 73.3%; Pred. No. 8.3;
Matches 11; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 GAARASGP-GGGAPR 14
Db 92 GAAPGRGPRGGAPR 106

RESULT 9
US-11-072-512-3295
; Sequence 3295, Application US/11072512
; Publication No. US20060029945A1

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```

; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: TSONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3295
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3295

Query Match 62.8%; Score 46.5; DB 7; Length 678;
Best Local Similarity 61.1%; Pred. No. 38;
Matches 11; Conservative 1; Mismatches 1; Indels 5; Gaps 1;

QY 1 GAA-----RASGPGGAP 13
Db 584 GAAKPPRPRAGPGGGWP 601

RESULT 10
US-11-096-568A-23806
; Sequence 23806, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23806
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(134)
; OTHER INFORMATION: Ceres Seq. ID no. 12415289
US-11-096-568A-23806

Query Match 62.2%; Score 46; DB 7; Length 134;
Best Local Similarity 72.7%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 ARASGPGGGAP 13
Db 69 ARGAGPGGAGAP 79

```


; LENGTH: 298

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-821-234-1240

Query Match 59.5%; Score 44; DB 6; Length 298;

Best Local Similarity 64.3%; Pred. No. 39;

Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAARASGPGGAPR 14

Db 133 GPARPLGGPAPR 146

Search completed: March 13, 2006, 20:03:30

Job time : 9.55294 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 13, 2006, 18:52:59 ; Search time 97.8924 seconds
(without alignments)
58.355 Million cell updates/sec

Title: US-09-529-206E-28
Perfect score: 68
Sequence: 1 AARASPGGGAPR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	68	100.0	13	2	AAY06064 Human can
2	68	100.0	14	2	AAY05986 Human can
3	68	100.0	15	2	AAY05978 Human can
4	68	100.0	20	2	AAY05979 Human can
5	68	100.0	30	5	AAY05105 Human NYN
6	68	100.0	179	8	ADK68648 Epitope 1
7	68	100.0	180	2	AAW62584 Cancer as
8	68	100.0	180	2	AAW69665 Human NY-
9	68	100.0	180	2	AAW05965 Human can
10	68	100.0	180	3	AAW52430 Human tum
11	68	100.0	180	3	AAY70862 Human tum
12	68	100.0	180	3	AAW03154 Human oes
13	68	100.0	180	4	AAW69946 Human NY-
14	68	100.0	180	4	AAW67164 Amino aci
15	68	100.0	180	4	AAU01535 Human NY-
16	68	100.0	180	4	AAE07714 Human NY
17	68	100.0	180	5	AAU84818 Human NYN
18	68	100.0	180	5	AAU11543 Human tum
19	68	100.0	180	6	ABR58672 Human can
20	68	100.0	180	6	ABR48210 Human bla
21	68	100.0	180	6	ABU56508 Lung can
22	68	100.0	180	6	ABU56694 Lung can
23	68	100.0	180	6	ABP74198 Human NY-
24	68	100.0	180	6	ABU64816 Human NY-

25	68	100.0	180	6	ABR83438 Human NY-
26	68	100.0	180	7	ADC09576 NY-ESO-1
27	68	100.0	180	7	ADD35564 Human NY-
28	68	100.0	180	7	ADD35568 Human NY-
29	68	100.0	180	7	ADD25510 Binding d
30	68	100.0	180	7	ADN39068 Cancer/an
31	68	100.0	180	8	ADJ54139 Human NY-
32	68	100.0	180	8	ADM72815 Human NY-
33	68	100.0	180	8	ADM73418 CAG-3 pro
34	68	100.0	180	8	ADM73417 Human NY-
35	68	100.0	180	8	ADQ18451 Human sof
36	68	100.0	180	8	ADQ10446 Autoimmun
37	68	100.0	180	8	ADS80926 Tumour as
38	68	100.0	180	9	ADM44353 Human aut
39	68	100.0	180	9	ADY85096 Tumour ant
40	68	100.0	180	9	ADZ28913 NY-ESO-1
41	68	100.0	180	9	ADZ42374 Immunogen
42	68	100.0	180	9	AEA35651 Human NY-
43	68	100.0	240	9	ADW99402 NY-ESO-1/
44	68	100.0	240	9	AE880047 Human NY-
45	68	100.0	397	4	AAE13122 NY-ESO-IC

ALIGNMENTS

RESULT 1
AAY06064
ID AAY06064 standard; peptide; 13 AA.
XX
AC AAY06064;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 peptide.
XX

NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
uterine cancer; breast cancer; prostate cancer; ovarian cancer;
cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
vaccine; cytotoxic T lymphocyte; CTL.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Example 11; Page 50; 88pp; English.
XX

This peptide corresponds to amino acid residues 50-62 of human NY ESO-1/CAG-3 ORP1 (see AAY05965), a new and potent tumour antigen that is capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,

CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 CC as breast, prostate, ovarian, pancreatic and thyroid cancers
 XX
 EQ Sequence 13 AA;

Query Match 100.0%; Score 68; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AARASGPGGGAPR 13
 |||||
 Db 1 AARASGPGGGAPR 13

RESULT 2
 AAY05986
 ID AAY05986 standard; peptide; 14 AA.
 XX
 AC AAY05986;

XX 16-AUG-1999 (first entry)

XX Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine.

XX Homo sapiens.

XX WO9918206-A2.

XX 15-APR-1999.

XX 21-SEP-1998; 98WO-US019609.

XX 08-OCT-1997; 97US-0061428P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang RF, Rosenberg SA;

XX WPI; 1999-277270/23.

XX Cancer antigen NY ESO1/CAG-3.

XX Claim 25; Page 50; 88pp; English.

XX The present sequence represents a cancer peptide that corresponds to
 CC amino acid residues 49-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
 CC AAY05965), a new and potent tumour antigen capable of eliciting an
 CC antigen specific immune response by T cells. Cancer peptides derived from
 CC CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
 CC variants (see AAY05967-87), are useful as cancer vaccines that protect
 CC against cancer. The invention provides: vectors and host cells (also
 CC useful as vaccines); a method of diagnosis of cancer or precancer; a
 CC transgenic animal; antisense oligonucleotides that inhibit expression of
 CC the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
 CC cancer peptide, useful in diagnostic and detection assays; and methods
 CC for preventing or inhibiting cancer by administering a cancer peptide,
 CC with or without an HLA molecule. The cancer peptides form part of, or are
 CC derived from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
 CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
 CC treated by inducing cancer-specific T cells in vitro for subsequent
 CC return to a patient

XX Sequence 14 AA;

Query Match 100.0%; Score 68; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AARASGPGGGAPR 13
 |||||
 Db 2 AARASGPGGGAPR 14

RESULT 3

AAY05978

ID AAY05978 standard; peptide; 15 AA.

XX

AC AAY05978;

XX 16-AUG-1999 (first entry)

XX Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine.

XX Homo sapiens.

XX WO9918206-A2.

XX 15-APR-1999.

XX 21-SEP-1998; 98WO-US019609.

XX 08-OCT-1997; 97US-0061428P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang RF, Rosenberg SA;

XX WPI; 1999-277270/23.

XX Cancer antigen NY ESO1/CAG-3.

XX Claim 15; Page 64; 88pp; English.

XX The present sequence represents a cancer peptide that corresponds to
 CC amino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
 CC AAY05965), a new and potent tumour antigen capable of eliciting an
 CC antigen specific immune response by T cells. Cancer peptides derived from
 CC CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
 CC variants (see AAY05967-87), are useful as cancer vaccines that protect
 CC against cancer. The invention provides: vectors and host cells (also
 CC useful as vaccines); a method of diagnosis of cancer or precancer; a
 CC transgenic animal; antisense oligonucleotides that inhibit expression of
 CC the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
 CC cancer peptide, useful in diagnostic and detection assays; and methods
 CC for preventing or inhibiting cancer by administering a cancer peptide,
 CC with or without an HLA molecule. The cancer peptides form part of, or are
 CC derived from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
 CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
 CC treated by inducing cancer-specific T cells in vitro for subsequent
 CC return to a patient

XX Sequence 15 AA;

Query Match 100.0%; Score 68; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AARASGPGGAPR 13
 DB 3 AARASGPGGAPR 15

RESULT 4
 ID AAY05979
 AC AAY05979 standard; peptide; 20 AA.
 XX
 DT 16-AUG-1999 (first entry)
 DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
 XX
 KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN W09918206-A2.
 XX
 PD 15-APR-1999.
 XX
 XX 21-SEP-1998; 98WO-US019609.
 XX
 PF 08-OCT-1997; 97US-0061428P.
 XX
 PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PA Wang RF, Rosenberg SA;
 PI WPI; 1999-277270/23.
 XX
 DR Cancer antigen NY ESO1/CAG-3.
 XX
 FT Claim 16; Page 64; 88pp; English.
 XX
 PS The present sequence represents a cancer peptide that is based on amino
 CC acid residues 44-62 of human ESO-1/CAG-3 (for CAG-3) ORF1 (see AAY05965),
 CC a new and potent tumour antigen capable of eliciting an antigen specific
 CC immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-
 CC 3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-
 CC 87), are useful as cancer vaccines that protect against cancer. The
 CC invention provides: vectors and host cells (also useful as vaccines); a
 CC method of diagnosis of cancer or precancer; a transgenic animal;
 CC antisense oligonucleotides that inhibit expression of the cancer peptide
 CC or tumour antigen; antibodies reacting with a CAG-3 cancer peptide,
 CC useful in diagnostic and detection assays; and methods for preventing or
 CC inhibiting cancer by administering a cancer peptide, with or without an
 CC HLA molecule. The cancer peptides form part of, or are derived from,
 CC cancers such as primary or metastatic melanoma, thymoma, lymphoma,
 CC sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
 CC cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
 CC prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by
 CC inducing cancer-specific T cells in vitro for subsequent return to a
 CC patient
 XX
 SQ Sequence 20 AA;
 Query Match 100.0%; Score 68; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AARASGPGGAPR 13
 DB 3 AARASGPGGAPR 15

RESULT 5
 ID AAU85105 standard; peptide; 30 AA.
 XX
 AC AAU85105;
 XX
 DT 08-MAY-2002 (first entry)
 DE Human NYNSOla segment 4.
 XX
 KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
 KW viral infection; human immunodeficiency virus; melanoma;
 KW bacterial infection; Salmonella; Legionella; parasitic infection;
 KW Trypanosoma; Toxoplasma; Giardia.
 XX
 OS Homo sapiens.
 XX
 PN W0200190197-A1.
 XX
 PD 29-NOV-2001.
 XX
 XX 25-MAY-2001; 2001WO-AU000622.
 XX
 PF 26-MAY-2000; 2000AU-00007761.
 XX
 PR (AUSU) UNIV AUSTRALIAN NAT.
 XX
 PA Thomson SA, Ramshaw IA;
 PI WPI; 2002-147575/19.
 XX
 DR N-PSDB; ABK36925.
 XX
 PT New synthetic polypeptides having several different segments of at least
 CC one parent polypeptide linked together differently compared to the
 CC linkage in the parent polypeptide, for inducing immune response against a
 CC pathogen or cancer.
 XX
 PS Example 3; Fig 27; 364pp; English.
 XX
 FT The invention relates to a new synthetic polypeptide (I) comprising
 CC several different segments of at least one parent polypeptide linked
 CC together in a different relationship relative to their linkage in the
 CC parent polypeptide to impede, abrogate or otherwise alter at least one
 CC function associated with the parent polypeptide and for inducing an
 CC immune response against a pathogen or cancer. Also included are a
 CC synthetic polynucleotide encoding and a computer system for designing the
 CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
 CC are referred to as a Savine. The synthetic polypeptide is useful for
 CC modulating immune responses preferably directed against a pathogen or a
 CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
 CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
 CC oesophagus, brain, testicle, uterus), as potentiating agents.
 CC Compositions comprising the polypeptide may be used in the treatment or
 CC prophylaxis against viral (such as infections caused by HIV (human
 CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
 CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
 CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
 CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
 CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
 CC a peptide derived from a parent protein used to construct a savine of the
 CC invention
 XX
 SQ Sequence 30 AA;
 Query Match 100.0%; Score 68; DB 5; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.034;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AARASGPGGAPR 13

```

Eb          |||||
            7 AARASGPGGAPR 19

RESULT 6
ADK68648
ID ADK68648 standard; protein; 179 AA.
XX
AC ADK68648;
XX
XX
DT 06-MAY-2004 (first entry)
XX
DE Epitope liberation-related NY-ESO-1 protein SeqID11.
XX
XX epitope liberation; substrate; proteasome; cytostatic; antibacterial;
KW protozoa; fungicide; T-cell activator; vaccine; housekeeping epitope;
KW cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;
KW virus; bacterium; protozoan; fungus; housekeeping proteasome system;
KW human.
XX
XX Homo sapiens.
XX
XX US2003228634-A1.
XX
XX 11-DEC-2003.
XX
XX 07-NOV-2002; 2002US-00292413.
XX
XX 07-NOV-2001; 2001US-0336968P.
XX
XX (SIMA/) SIMARD J J L.
PA (DIAM/) DIAMOND D C.
PA (CIUZ/) QIU Z.
PA (LEIX/) LEI X.
XX
XX Simard J J L, Diamond DC, Qiu Z, Lei X;
XX
XX WPI; 2004-167209/16.
DR N-PSDB; ADK68674.
XX
XX Identifying polypeptide suitable for epitope e.g., housekeeping epitope,
PT liberation by contacting substrate polypeptide comprising epitope of
PT interest, with proteasome, and assaying for liberation of epitope.
XX
XX Example 2; SEQ ID NO 11; 67pp; English.
XX
XX This invention relates to a novel method of identifying a polypeptide
CC suitable for epitope liberation, including the steps of identifying an
CC epitope of interest; providing substrate polypeptide sequence including
CC the epitope, wherein the substrate permits processing by a proteasome;
CC contacting the substrate with a composition including the proteasome,
CC under conditions that support processing of the substrate by proteasome;
CC and assaying for liberation of epitope. The invention may be useful for
CC the development of compounds with a cytostatic, antibacterial,
CC protozoa or fungicide activity acting as T-cell activators. In
CC addition, the invention may allow development of a vaccine. The invention
CC is useful for identifying a polypeptide suitable for epitope liberation,
CC where the epitope is a housekeeping epitope. The compositions comprising
CC the identified housekeeping epitopes are useful in vitro in vaccine
CC development or in the generation or expansion of cytotoxic T lymphocyte
CC (CTL) to be used in adoptive immunotherapy. The invention is also useful
CC for activating T-cells against neoplastic cells, and cells infected with
CC virus, bacterium, protozoan or fungus. CTL epitopes are identified based
CC on the knowledge that such epitopes are, in fact, produced by the
CC housekeeping proteasome system. Once identified, these epitopes, embodied
CC as peptides, can be used to successfully immunise or induce therapeutic
CC CTL responses against housekeeping proteasome expressing target cells in
CC the host. The present sequence is that of a protein which is related to
CC the method of the invention.
XX
XX SQ Sequence 179 AA;
Query Match 100.0%; Score 68; DB 8; Length 179;

Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AARASGPGGAPR 13
   |||||
Db 49 AARASGPGGAPR 61

RESULT 7
AAW62584
ID AAW62584 standard; protein; 180 AA.
XX
AC AAW62584;
XX
XX 17-SEP-1998 (first entry)
DT
DE Cancer associated antigen NY-ESO-1.
XX
KW Cancer associated antigen; NY-ESO-1; regression; progression; onset;
KW cancer; treatment; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Misc-difference 7 /note= "potential myristoylation site"
FT Misc-difference 9 /note= "potential myristoylation site"
FT Misc-difference 11 /note= "potential phosphorylation site"
FT Misc-difference 98 /note= "potential phosphorylation site"
FT Misc-difference 134 /note= "potential phosphorylation site"
FT Misc-difference 138 /note= "potential phosphorylation site"
XX
XX WO9814464-A1.
XX
XX 09-APR-1998.
XX
XX 15-SEP-1997; 97WO-US016335.
XX
XX 03-OCT-1996; 96US-00725182.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Chen Y, Scanlan M, Gure A, Old LJ, Jager E, Knuth A;
PI Drijfhout JW;
XX
XX WPI; 1998-286417/25.
DR N-PSDB; AAW38566.
XX
XX New isolated cancer associated antigen - is used to develop products for
PT the diagnosis and treatment of cancers and for monitoring cancer therapy.
XX
XX Claim 8; Fig 3; 49pp; English.
XX
XX The present sequence represents a cancer associated antigen. The clone
CC from which the DNA sequence is obtained is designated NY-ESO-1. The
CC specification described a method for determining regression, progression
CC of onset of a cancerous condition, comprising monitoring a sample from a
CC patient with the cancerous condition for a parameter selected from NY-ESO
CC -1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells
CC specific for the peptide and an MHC molecule with which it non-covalently
CC complexes. Methods for the treatment of a cancerous condition are also
CC described. The NY-ESO-1 protein and peptides derived from it can be used
CC for diagnosis and treatment of cancers and to monitor the efficacy of a
CC therapeutic regime
XX
XX SQ Sequence 180 AA;
Query Match 100.0%; Score 68; DB 2; Length 180;

```

Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AARASGPGGAPR 13
| | | | | | | | | |
Db 50 AARASGPGGAPR 62

RESULT 8

AAW69665
ID AAW69665 standard; protein; 180 AA.

AC AAW69665;

DT 27-OCT-1998 (first entry)

DE Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.

XX Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.

OS Homo sapiens.

PN W09832855-A1.

PD 30-JUL-1998.

XX 27-JAN-1998; 98WO-US001445.

PF 27-JAN-1997; 97US-00791495.

PR (LUDW-) LUDWIG INST CANCER RES.

XX Lethe B, Lucas S, De Smet C, Godelaine D, Boon-talleur T;

XX WPI; 1998-427951/36.

DR N-PSDB; AAV50348.

XX New isolated LAGE-1 tumour associated nucleic acids - used to develop products for the diagnosis and treatment of LAGE-1 associated disorders, particularly tumours.

PS Example 2; Page 57-58; 73pp; English.

XX The present sequence represents human NY-ESO-1, formerly known as LL-1.2 clone, which is used in an example from the present invention which describes LAGE-1 tumour associated protein (TAP). The present invention also describes: (1) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering to the subject autologous cytolytic T cells to ameliorate the disorder, where the cytolytic T cells are specific for complexes of an HLA molecule and a LAGE-1 TAP or an immunogenic fragment; (2) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering a LAGE-1 TAP or an immunogenic fragment to ameliorate the disorder; and (3) a method for selectively enriching a population of T cells with cytolytic T cells specific for a LAGE-1 TAP comprising contacting an isolated population of T cells with an agent presenting a complex of a LAGE TAP or an immunogenic fragment and a HLA presenting molecule to selectively enrich the isolated population of T cells with the cytolytic T cells. The methods and products from the present invention can be used for the diagnosis and treatment of LAGE-1 associated disorders, particularly tumours

SQ Sequence 180 AA;

Query Match 100.0%; Score 68; DB 2; Length 180;

Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AARASGPGGAPR 13
| | | | | | | | | |
Db 50 AARASGPGGAPR 62

RESULT 9

AAV05965

ID AAV05965 standard; protein; 180 AA.

XX AAV05965;

AC 16-AUG-1999 (first entry)

DT Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; ORF1.

OS Homo sapiens.

PN W09918206-A2.

PD 15-APR-1999.

XX 21-SEP-1998; 98WO-US019609.

PF 08-OCT-1997; 97US-0061428P.

PR (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang RF, Rosenberg SA;

XX WPI; 1999-277270/23.

DR N-PSDB; AAX58599.

XX Cancer antigen NY ESO1/CAG-3.

PT Claim 4; Fig 3A; 88pp; English.

XX The present sequence represents the ORF1 protein encoded by open reading frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides comprising ORF1, ORF2 (see AAV05966), portions of these peptides and their variants (see AAV05965-87), are useful as cancer vaccines that protect the recipient from development of cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with the CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent return to a patient

XX Sequence 180 AA;

Query Match 100.0%; Score 68; DB 2; Length 180;

Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AARASGPGGAPR 13

Db 50 AARASGPGGAPR 62

RESULT 10

AAV52430

ID	AA52430	standard; protein; 180 AA.
XX		
AC	AA52430;	
XX		
ET	21-OCT-2004 (revised)	
LT	15-FEB-2000 (first entry)	
XX		
XX	Human tumour antigen NY-ESO-1.	
DE		
XX		
KW	Cancer; tumour; antigen; MHC; major histocompatibility complex; T-cell;	
KW	cytotoxic; helper; stimulation; proliferation; treatment; diagnosis;	
KW	prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;	
KW	hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.	
XX		
OS	Homo sapiens.	
OS	Unidentified.	
XX		
PH	Key	Location/Qualifiers
PT	Peptide	44..53
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-B7"
PT	Peptide	60..69
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-B7"
PT	Peptide	60..68
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-B7"
PT	Peptide	63..72
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-B7"
PT	Peptide	79..88
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-B7"
PT	Peptide	79..87
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-B7, HLA-B8 and HLA-B35"
PT	Peptide	82..91
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-A1"
PT	Peptide	82..90
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-A1"
PT	Peptide	83..91
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-B44"
PT	Peptide	84..92
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-B7, HLA-B8 and HLA-B35"
PT	Peptide	87..96
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-A1"
PT	Peptide	88..96
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-B44"
PT	Peptide	96..104
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-B7"
PT	Peptide	100..108
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-B44"
PT	Peptide	102..110
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-B44"
PT	Peptide	107..116
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-A24"
PT	Peptide	110..118
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-B52"
PT	Peptide	113..122
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-B7 and HLA-B52"
PT	Peptide	113..121
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-B7"
PT	Peptide	115..124
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-A3"
PT	Peptide	118..126
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-B35"
PT	Peptide	124..133
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-B52"
PT	Peptide	125..133
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-A24"
PT	Peptide	138..147
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-B8"
PT	Peptide	139..147
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-B7"
PT	Peptide	145..153
PT	Peptide	/note= "Peptide presented by MHC Class I HLA-A24 and HLA-

FT	Peptide	B52"
FT	Peptide	153..162
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-B52"
FT	Peptide	154..163
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-B52"
FT	Peptide	154..162
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-B52"
FT	Peptide	156..167
FT	Peptide	/note= "Peptide (AA52434) presented by MHC Class I HLA-A2"
FT	Peptide	158..166
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-A3"
FT	Peptide	159..167
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-A3"
FT	Peptide	162..170
FT	Peptide	/note= "Peptide presented by MHC Class I HLA-B52"
XX		
PN	WO9953938-A1.	
XX		
PD	28-OCT-1999.	
XX		
PF	24-MAR-1999; 99WO-US006875.	
XX		
PR	17-APR-1998; 98US-00062422.	
PR	02-OCT-1998; 98US-00165546.	
XX		
PA	(LUDW-) LUDWIG INST CANCER RES.	
XX		
PI	Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;	
PI	Gure A, Ritter G;	
XX		
DR	WPI; 2000-038483/03.	
DR	N-PSDB; AAZ38380.	
XX		
PT	Novel peptides which bind to MHC class I and MHC class II molecules,	
PT	useful for therapeutic and diagnostic purposes.	
XX		
PS	Claim 30; Fig 3; 49pp; English.	
XX		
CC	This sequence represents a human tumour antigen, NY-ESO-1, the cDNA	
CC	encoding which was isolated from an oesophagus squamous cell cancer	
CC	library. Tissue localisation studies revealed it to be expressed at high	
CC	levels in normal ovary and testis but not in normal colon, kidney, liver,	
CC	brain, oesophagus and skin. It was expressed in certain tumours and	
CC	tumour cell lines with some degree of frequency - these included melanoma	
CC	specimens and cell lines, and breast and bladder cancer specimens, with	
CC	expression in other tumour types being sporadic. Peptides derived from NY	
CC	-ESO-1 are bound by both MHC (major histocompatibility complex) Class I	
CC	and Class II molecules for presentation to T-cells. Peptides AA52431-	
CC	Y52434 bind to Class I HLA-A2 molecules, thereby stimulating	
CC	proliferation of cytotoxic T-cells, while peptides AA52435-Y52440 bind	
CC	to Class II HLA-DR53 molecules, stimulating helper T-cell proliferation.	
CC	The peptides derived from NY-ESO-1 may be used in methods and	
CC	compositions used for the treatment, diagnosis and prevention of cancers	
CC	(such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma,	
CC	ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to	
CC	stimulate the proliferation of T cells	
CC		
CC	Revised record issued on 21-OCT-2004 : Correction to feature table key	
XX		
SQ	Sequence 180 AA;	
CC		
CC	Query Match 100.0%; Score 68; DB 3; Length 180;	
CC	Best Local Similarity 100.0%; Pred. No. 0.16;	
XX	Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 AARASGPGGAPR 13	
Db	50 AARASGPGGAPR 62	
RESULT 11		
AA570862		

```

ID XX AAY70862 standard; protein; 180 AA.
AC XX
XX XX
DT XX AAY70862;
XX XX
DE XX 31-JUL-2000 (first entry)
XX XX
XX XX Human tumour antigen, NY-ESO-1 protein.
XX XX
XX XX NY-ESO-1; CAMEL; CTL-recognised Antigen on MELANOMA; human; cancer; CTL;
XX XX cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer;
XX XX melanoma; immunotherapy; immune response.
XX XX
XX XX Homo sapiens.
XX XX
XX XX WO200023584-A1.
XX XX
XX XX 27-APR-2000.
XX XX
XX XX 15-OCT-1999; 99WO-EP007832.
XX XX
XX XX 16-OCT-1998; 98EP-00119583.
XX XX
XX XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX XX (UYHO-) UNIV HOSPITAL LEIDEN.
XX XX
XX XX Schrier PI, Aarnoudse CA, Heider K, Klade C;
XX XX
XX XX WPI; 2000-339685/29.
XX XX
XX XX N-PSDB; AAD00152.
XX XX
XX XX Tumour-associated antigen useful for cancer immunotherapy is encoded by
XX XX the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
XX XX
XX XX Example 3; Page 62-63; 73pp; English.
XX XX
XX XX The present sequence is the human NY-ESO-1 protein, a tumour antigen,
XX XX identified by screening an esophagus carcinoma cDNA library. This protein
XX XX is derived from open reading frame (ORF)-1 that contain epitopes of
XX XX tumour specific T-cells. NY-ESO-1 is expressed in different tumour types,
XX XX but not in healthy tissues except in testis. It also shows homology with
XX XX the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELANOMA)
XX XX protein, a tumour-associated antigen. The tumour-associated antigen
XX XX displayed on melanoma cells is recognised by cytotoxic T lymphocytes.
XX XX This sequence has anticancer activity. CAMEL tumour antigen and
XX XX immunogenic peptides derived from it are useful for cancer immunotherapy.
XX XX They have the potential to induce an immune response, by eliciting a CTL
XX XX response. The DNA molecule is used for the construction of recombinant or
XX XX fusion proteins
XX XX
XX XX Sequence 180 AA;
XX XX
XX XX Query Match 100.0%; Score 68; DB 3; Length 180;
XX XX Best Local Similarity 100.0%; Pred. No. 0.16;
XX XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX XX Qy 1 AARASGPGGAPR 13
XX XX |||||
XX XX Db 50 AARASGPGGAPR 62
XX XX
XX XX RESULT 12
XX XX AAB03154
XX XX ID AAB03154 standard; protein; 180 AA.
XX XX
XX XX AC AAB03154;
XX XX
XX XX 23-OCT-2000 (first entry)
XX XX
XX XX Human oesophageal cancer-associated antigen NY-ESO-1.
XX XX
XX XX Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen;
XX XX oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain;
XX XX antibody; diagnostic marker; drug delivery target.

```

```

XX OS Homo sapiens.
XX XX
XX XX Key Location/Qualifiers
XX XX Modified-site 7 /note= "Potential N-myristoylation site"
XX XX Modified-site 9 /note= "Potential N-myristoylation site"
XX XX Modified-site 11 /note= "Potential O-phosphorylation site"
XX XX Modified-site 98 /note= "Potential O-phosphorylation site"
XX XX Modified-site 134 /note= "Potential O-phosphorylation site"
XX XX Modified-site 138 /note= "Potential O-phosphorylation site"
XX XX Domain 152..172 /note= "Potential transmembrane domain"
XX XX
XX XX US6069233-A.
XX XX
XX XX 30-MAY-2000.
XX XX
XX XX 26-JAN-1998; 98US-00013150.
XX XX
XX XX 03-OCT-1996; 96US-00725381.
XX XX
XX XX (SLOK ) SLOAN KETTERING INST CANCER RES.
XX XX (CORR ) CORNELL RES FOUND INC.
XX XX (LUDW-) LUDWIG INST CANCER RES.
XX XX
XX XX Scanlan M, Gure AO, Chen Y, Tureci O, Sahin U, Pfreundschuh M;
XX XX Old LJ;
XX XX
XX XX WPI; 2000-410880/35.
XX XX N-PSDB; AAA61483.
XX XX
XX XX New isolated esophageal cancer-associated antigen useful as markers for
XX XX producing antibodies and as targets for identifying abnormal conditions,
XX XX e.g. infections and cancer.
XX XX
XX XX Example 5; Fig 3; 9pp; English.
XX XX
XX XX This sequence represents a human oesophageal cancer-associated antigen,
XX XX NY-ESO-1. The cDNA encoding this sequence was isolated from a cDNA
XX XX library prepared from a specimen of well-to-moderately differentiated
XX XX squamous cell cancer of the oesophagus. Expression analysis demonstrated
XX XX that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma
XX XX cell lines and in normal ovary and testis tissue, but not in normal
XX XX colon, kidney, liver or brain tissue. Analysis of the amino acid sequence
XX XX of the protein indicates that the protein has a transmembrane domain,
XX XX several N-myristoylation sites and O-phosphorylation sites and that it
XX XX contains antigenic sequences in the N-terminal half of the protein. The
XX XX antigen is useful as an immunogen when combined with an adjuvant, in both
XX XX precursor and post- translationally modified forms, and may be used to
XX XX generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic
XX XX marker for oesophageal cancer, and can be utilised as a marker for the
XX XX targetted delivery of therapeutic agents to oesophageal cancer cells. It
XX XX can also be used to generate diagnostic or therapeutic agents
XX XX
XX XX Sequence 180 AA;
XX XX
XX XX Query Match 100.0%; Score 68; DB 3; Length 180;
XX XX Best Local Similarity 100.0%; Pred. No. 0.16;
XX XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX XX Qy 1 AARASGPGGAPR 13
XX XX |||||
XX XX Db 50 AARASGPGGAPR 62
XX XX
XX XX RESULT 13
XX XX AAB69946

```

ID AAB69946 standard; protein; 180 AA.
 AC AAB69946;
 XX
 DT 27-APR-2001 (first entry)
 XX
 XX Human NY-ESO-1 protein.
 DE
 XX Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
 KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
 KW non-small cell lung carcinoma; tumour status determination.
 XX
 CS Homo sapiens.
 XX
 XX WO200107917-A1.
 PN
 XX
 PD 01-FEB-2001.
 XX
 XX 14-JUL-2000; 2000WO-US019220.
 PF
 XX 23-JUL-1999; 99US-00359503.
 FR
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (CORR) CORNELL RES FOUND INC.
 XX
 XX Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
 PI
 XX WPI; 2001-182822/18.
 DR N-PSDB; AAF58634.
 DR
 XX Method useful for determining the status (e.g. progression, regression or
 PT stability of the disease) of a cancerous condition, involves determining
 PT the levels of NY-ESO-1 specific antibodies in a sample taken from a
 PT patient.
 XX
 PS Example 5; Fig 3; 50pp; English.
 XX
 XX The present sequence is human NY-ESO-1 protein. It is provided in a
 CC specification relating to a method for determining the status of a
 CC cancerous condition in a patient with a tumour that expresses NY-ESO-1.
 CC The method comprises assaying a sample taken from the patient for
 CC antibodies that specifically bind to the NY-ESO-1 and comparing the value
 CC obtained to a prior value obtained from assay of a prior sample taken
 CC from the patient. Any difference between the values is indicative of a
 CC change in status of the cancerous condition. The method is useful for
 CC determining whether a cancerous condition is progressing, regressing or
 CC remaining stable, in particular in patients receiving treatment for a
 CC melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
 CC carcinoma
 XX
 XX Sequence 180 AA;
 SQ

Query Match 100.0%; Score 68; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AARASGPGGGAPR 13
 DB 50 AARASGPGGGAPR 62
 |||||
 RESULT 15
 AAU01535
 ID AAU01535 standard; protein; 180 AA.
 XX
 AC AAU01535;
 XX
 XX 18-JUL-2001 (first entry)
 DT
 XX
 DE Human NY-ESO-1 tumour rejection antigen precursor protein.
 XX
 XX NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
 KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
 KW human leukocyte antigen-determining region; disease progression;
 KW disease regression; disease onset; body tissue; body fluid; enzyme label;
 KW radioactive label; monoclonal antibody.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FT Modified-site 7
 FT /note= "Myristoylated"
 FT Modified-site 9
 FT /note= "Myristoylated"
 FT Modified-site 11
 FT /note= "Phosphorylated"
 FT Modified-site 98
 FT /note= "Phosphorylated"
 FT Modified-site 134
 FT /note= "Phosphorylated"
 FT

RESULT 14
 AAG67164
 ID AAG67164 standard; protein; 180 AA.
 XX
 AC AAG67164;
 XX
 XX 13-NOV-2001 (first entry)
 DT
 XX Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
 DE
 XX Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
 KW

KW HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour;
 KW cancer; testis tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200162917-A1.
 XX
 PD 30-AUG-2001.
 XX
 XX 22-JAN-2001; 2001WO-US002126.
 PF
 XX 22-FEB-2000; 2000US-00510635.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX Lethe B, Boon-Falleur T;
 PI
 XX WPI; 2001-550091/61.
 DR N-PSDB; AAH75118.
 DR
 XX Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful
 PT for diagnosing testicular tumors.
 PT
 XX Example 5; Fig 3; 50pp; English.
 XX
 XX The present sequence represents cancer testis tumour antigen NY-ESO-1
 CC (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at
 CC least one human leukocyte antigen (HLA) binding peptide, which binds to
 CC Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is
 CC expressed in tumour mRNA and in testis, but not normal colon, kidney,
 CC liver or brain tissue. The presence or level of expression of NY-ESO-1
 CC may be assayed for the diagnosis of cancer, especially testis tumours
 XX
 XX Sequence 180 AA;
 SQ

Query Match 100.0%; Score 68; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 AARASGPGGGAPR 13
 DB 50 AARASGPGGGAPR 62
 |||||
 RESULT 15
 AAU01535
 ID AAU01535 standard; protein; 180 AA.
 XX
 AC AAU01535;
 XX
 XX 18-JUL-2001 (first entry)
 DT
 XX
 DE Human NY-ESO-1 tumour rejection antigen precursor protein.
 XX
 XX NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
 KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
 KW human leukocyte antigen-determining region; disease progression;
 KW disease regression; disease onset; body tissue; body fluid; enzyme label;
 KW radioactive label; monoclonal antibody.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FT Modified-site 7
 FT /note= "Myristoylated"
 FT Modified-site 9
 FT /note= "Myristoylated"
 FT Modified-site 11
 FT /note= "Phosphorylated"
 FT Modified-site 98
 FT /note= "Phosphorylated"
 FT Modified-site 134
 FT /note= "Phosphorylated"
 FT

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GenCore version 5.1.7
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OM protein - protein search, using sw model
Run on: March 13, 2006, 19:04:24 ; Search time 15,4471 Seconds
(without alignments)
80.975 Million cell updates/sec

Title: US-09-529-206E-28

Perfect score: 68

Sequence: 1 AARASGPGGGAPR 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80.*

1: PIR.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	64.7	82	T04476	acclimation protei
2	44	64.7	286	S04673	H+-transporting tw
3	44	64.7	379	A48082	MAP kinase 3 (BC 2
4	44	64.7	3190	T13828	CREB-binding prote
5	43	63.2	185	T36874	hypothetical prote
6	43	63.2	213	S42585	DNA-invertase - Rh
7	43	63.2	222	T36115	probable oxidoredu
8	43	63.2	349	S55626	hypothetical prote
9	43	63.2	377	T28184	Ca2+/calmodulin-de
10	43	63.2	380	JC1451	regulatory protein
11	43	63.2	679	S02165	regulatory protein
12	43	63.2	954	A87431	peptidyl-tRNA hydr
13	42	61.8	143	H87399	hypothetical prote
14	42	61.8	201	T2	hypothetical prote
15	42	61.8	337	T29031	hypothetical prote
16	42	61.8	335	S08341	myristylated alani
17	42	61.8	351	S50754	hypothetical prote
18	42	61.8	378	C87425	aldose 1-epimerase
19	42	61.8	387	T52451	endopeptidase Clp
20	42	61.8	436	T36104	conserved hypothet
21	42	61.8	474	T75580	conserved hypothet
22	42	61.8	1690	T35694	ATP dependent DNA
23	41.5	61.0	521	A29345	steroid hormone re
24	41	60.3	134	AB2695	hypothetical prote
25	41	60.3	134	B97477	hypothetical prote
26	41	60.3	173	F83648	flagellar basal-bo
27	41	60.3	357	F82878	XAA-PRO aminopepti
28	41	60.3	371	T39312	hypothetical prote
29	41	60.3	389	T15102	hypothetical prote

30 41 60.3 505 2 S68518 tub protein, brain
31 41 60.3 627 2 A44112 spidroin 2, dragli
32 41 60.3 1207 2 T00378 KIAA0641 protein -
33 40 58.8 190 1 JWBT DNA-invertase - Sa
34 40 58.8 290 2 T36712 hypothetical prote
35 40 58.8 291 1 S31415 glycine-rich prote
36 40 58.8 294 2 T17265 hypothetical prote
37 40 58.8 383 2 A86182 hypothetical prote
38 40 58.8 575 2 A47214 JK-recombination s
39 40 58.8 910 2 A34721 androgen receptor
40 40 58.8 911 2 B34721 androgen receptor
41 40 58.8 919 2 A39248 heterogeneus nucl
42 39.5 58.1 328 2 A44192 collagen alpha 1 c
43 39.5 58.1 730 2 A36226 tegument protein 6
44 39.5 58.1 3436 2 S55659 hypothetical prote
45 39 57.4 103 2 C72683

ALIGNMENTS

RESULT 1

T04476

acclimation protein 2 - barley

C:Species: Hordeum vulgare (barley)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: T04476

R:Phillips, J.R.; Dunn, M.A.; Hughes, M.A.

Plant Mol. Biol. 33, 1013-1023, 1997

A>Title: mRNA stability and localisation of the low temperature responsive barley gene

A:Reference number: Z15367; MUID:97299834; PMID:9154983

A:Accession: T04476

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-82 <PHI>

A:Cross-references: UNIPROT:Q40033; UNIPARC:UPI000009CE5A; EMBL:X97917; NID:G1418969; P

A:Experimental source: cv. Igri

C:Genetics:

A:Gene: btl14.2

Query Match 64.7%; Score 44; DB 2; Length 82;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AARASGPGGGAP 12

DB 32 AARGAGAGGGVP 43

RESULT 2

S04673

H+-transporting two-sector ATPase (EC 3.6.3.14) gamma chain - Rhodospseudomonas blastica

C:Species: Rhodospseudomonas blastica

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 31-Dec-2004

C:Accession: S04673

R:Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.

J. Mol. Biol. 179, 185-214, 1984

A>Title: Rhodospseudomonas blastica atp operon. Nucleotide sequence and transcription.

A:Reference number: S04666; MUID:85058188; PMID:6209404

A:Accession: S04673

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-286 <TYB>

A:Cross-references: UNIPROT:P05436; UNIPARC:UPI0000126582

C:Superfamily: H(+)-transporting ATP synthase gamma chain

C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

Query Match 64.7%; Score 44; DB 2; Length 286;

Best Local Similarity 69.2%; Pred. No. 40;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AARASGPGGGAPR 13

DB 32 AARGAGAGGGVP 43

Db 54 ASLASQGAGAPR 66

RESULT 3

MAP kinase 3 (EC 2.7.1.1) - human

N:Alternate names: extracellular signal-regulated kinase 1 (ERK1); mitogen-activated protein kinase (EC 2.7.1.37)

N:Contains: protein kinase (man)

C:Species: Homo sapiens

C>Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004

C:Accession: A48082; PQ0270; S23428; S15519; S21579

F:Charest, D.L.; Mordret, G.; Harder, K.W.; Jirik, F.; Pelech, S.L.

Nol. Cell. Biol. 13, 4679-4690, 1993

A:Title: Molecular cloning, expression, and characterization of the human mitogen-activated protein kinase 3

A:Reference number: A48082; MUID:93330262; PMID:7687743

A:Accession: A48082

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-379 <CHA>

A:Cross-references: UNIPROT:P27361; UNIPARC:UPI0000035BE2; EMBL:X60188; NID:g31220; PIDN:A48082

A:Experimental source: hepatoma cell line HEP G2

A>Note: authors translated the codon AGC for residue 174 as Ile

R:Owaki, H.; Makar, R.; Boulton, T.G.; Cobb, M.H.; Geppert, T.D.

Biochem. Biophys. Res. Commun. 182, 1416-1422, 1992

A:Title: Extracellular signal-regulated kinases in T cells: characterization of human ERK1 and ERK2

A:Reference number: JQ1400; MUID:92171961; PMID:1540184

A:Accession: PQ0270

A:Molecule type: mRNA

A:Residues: 14-173, 'I', 175-379 <OWA>

A:Cross-references: UNIPARC:UPI000016AB99; GB:M84490; NID:g186695; PIDN:AAA36142.1; PID:A48082

A:Experimental source: cell line CEM

R:Gonzalez, F.A.; Raden, D.L.; Rigby, M.R.; Davis, R.J.

FEBS Lett. 304, 170-178, 1992

A:Title: Heterogeneous expression of four MAP kinase isoforms in human tissues.

A:Reference number: S23426; MUID:92316223; PMID:1319925

A:Accession: S23428

A:Molecule type: mRNA

A:Residues: 25-173, 'I', 175-379 <CON>

A:Cross-references: UNIPARC:UPI000016A2B4; EMBL:Z11696; NID:g23892; PIDN:CAA77754.1; PID:A48082

C:Comment: This enzyme is activated by MAP kinase kinase (see PIR:45100 and PIR:A46723).

C:Genetics:

A:Gene: GDB:PRKM3; ERK1

A:Cross-references: GDB:135679; OMIM:601795

A:Map position: 16pter-16qter

C:Complex: monomer

C:Function:

A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate

A:Pathway: MAP kinase cascade

C:Superfamily: kinase-related transforming protein; protein kinase homology

C:Keywords: ATP; monomer; phosphoprotein; phosphotransferase; serine/threonine-specific kinase

F:40-330/Domain: protein kinase homology <KIN>

F:48-56/Region: protein kinase ATP-binding motif

F:202/Binding site: phosphate (Thr) (covalent) (by MAP kinase kinase) #status predicted

F:204/Binding site: phosphate (Tyr) (covalent) (by MAP kinase kinase) #status predicted

Query Match 64.7%; Score 44; DB 1; Length 379;

Best Local Similarity 69.2%; Pred. No. 51;

Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AARASGPGGAPR 13

Db 3 AAAAQCGGGGER 15

RESULT 4

T13828

CREB-binding protein homolog - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T13828

R:Akinaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; Go

Nature 386, 735-738, 1997

A:Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling.

A:Reference number: Z17785; MUID:97263578; PMID:9109493

A:Accession: T13828

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-3190 <AKI>

A:Cross-references: UNIPROT:O01368; UNIPARC:UPI000003EB83; EMBL:U88570; NID:g1916929; PID:A48082

C:Genetics:

A:Cross-references: FlyBase:FBgn0015624

A:Map position: X

F:1723-1780/Domain: bromodomain homology <BRO>

Query Match 64.7%; Score 44; DB 2; Length 3190;

Best Local Similarity 77.8%; Pred. No. 3.2e+02;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SGPGGGAPR 13

Db 320 NGPGGGGPR 328

RESULT 5

T36874

hypothetical protein SCI51.11c - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T36874

R:Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1999

A:Reference number: Z21617

A:Accession: T36874

A:Molecule type: DNA

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-185 <MUR>

A:Cross-references: UNIPROT:Q9S229; UNIPARC:UPI00000DB31A; EMBL:AL109848; PIDN:CA852835

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SCI51.11c

Query Match 63.2%; Score 43; DB 2; Length 185;

Best Local Similarity 72.7%; Pred. No. 38;

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AARASGPGGGA 11

Db 85 SARGSGPGSGA 95

RESULT 6

S42585

DNA-invertase - Rhizobium leguminosarum transposon Tn163

N:Alternate names: resolvase

C:Species: Rhizobium leguminosarum

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S42585

R:Ulrich, A.; Puhler, A.

Mol. Gen. Genet. 242, 505-516, 1994

A:Title: The new class II transposon Tn163 is plasmid-borne in two unrelated Rhizobium strains

A:Reference number: S42584; MUID:94166763; PMID:8121409

A:Accession: S42585

A:Molecule type: DNA

A:Residues: 1-213 <ULR>

A:Cross-references: UNIPROT:Q52760; UNIPARC:UPI00000AE947; EMBL:L14931; NID:g349099; PID:A48082

A:Experimental source: strain E163N; class II transposon Tn163

C:Genetics:

A:Gene: tnpR

A:Genome: transposon Tn163

C:Superfamily: transposase repressor

C:Keywords: DNA binding; DNA integration; DNA recombination

F:Fill/Active site: Ser #status predicted

Query Match 63.2%; Score 43; DB 2; Length 213;

Best Local Similarity 75.0%; Pred. No. 42;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AARASGPGGGAP 12
 |||||
 Db 137 AARARGNGGAP 148

RESULT 7
 T36115
 probable oxidoreductase - Streptomyces coelicolor
 C;Species: Streptomyces coelicolor
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
 C;Accession: T36115
 R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, April 1999
 A;Reference number: Z21597
 A;Accession: T36115
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-222 <MUR>
 A;Cross-references: UNIPROT:Q9X887; UNIPARC:UPI00000DB008; EMBL:AL049707; PIDN:CAB41281
 A;Experimental source: strain A3(2)
 C;Genetics:
 A;Gene: SCOEDB:SCE15.12C
 C;Superfamily: NAD(P)H-dependent FMN reductase (sulfate starvation-induced protein 4); S

Query Match 63.2%; Score 43; DB 2; Length 222;
 Best Local Similarity 66.7%; Pred. No. 44;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AARASGPGGGAP 12
 :|||||
 Db 182 SARASGPSAGRP 193

RESULT 8
 S55626
 hypothetical protein 32 - equine herpesvirus 2
 C;Species: equine herpesvirus 2
 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S55626
 R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
 J. Mol. Biol. 249, 520-528, 1995
 A;Title: The DNA sequence of equine herpesvirus 2.
 A;Reference number: S55594; MUID:95302501; PMID:7783207
 A;Accession: S55626
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-349 <TEL>
 A;Cross-references: UNIPROT:Q66635; UNIPARC:UPI00000EDFA7; GB:U20824; NID:G695172; PIDN:
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995

Query Match 63.2%; Score 43; DB 2; Length 349;
 Best Local Similarity 69.2%; Pred. No. 65;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AARASGPGGGAP 13
 |||||
 Db 34 AARASGPGGSGR 46

RESULT 9
 S28184
 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) erk-1 - mouse (fragment)
 N;Alternate names: extracellular signal-regulated kinase 1
 C;Species: Mus musculus (house mouse)
 C;Date: 22-Nov-1993 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
 C;Accession: S28184; B40466; A41371
 R;Tanner, B.; Mueckler, M.
 Biochim. Biophys. Acta 1171, 319-320, 1993
 A;Title: Molecular cloning of a mouse extracellular signal regulated kinase (erk-1).
 A;Reference number: S28184; MUID:93144347; PMID:8424957
 A;Accession: S28184
 A;Molecule type: mRNA

A;Residues: 1-377 <TAN>
 A;Cross-references: UNIPROT:Q63844; UNIPARC:UPI000017558C; EMBL:Z14249
 R;De Miguel, C.; Kligman, D.; Patel, J.; Detera-Wadleigh, S.D.
 DNA Cell Biol. 10, 505-514, 1991
 A;Title: Molecular analysis of microtubule-associated protein-2 kinase cDNA from mouse
 A;Reference number: A40466; MUID:91369479; PMID:1716439
 A;Accession: B40466
 A;Molecule type: mRNA
 A;Residues: 74-377 <DEM>
 A;Cross-references: UNIPARC:UPI0000023599; GB:S59517
 R;Crews, C.M.; Alessandrini, A.A.; Erikson, R.L.
 Proc. Natl. Acad. Sci. U.S.A. 88, 8845-8849, 1991
 A;Title: Mouse Erk-1 gene product is a serine/threonine protein kinase that has the pot
 A;Reference number: A41371; MUID:92020947; PMID:1717989
 A;Accession: A41371
 A;Molecule type: mRNA
 A;Residues: 7-16 <CRE>
 A;Cross-references: UNIPARC:UPI0000170C57; GB:SS8470; NID:G236372; PIDN:AAAB19973.1; PID
 C;Superfamily: kinase-related transforming protein; protein kinase homolog
 C;Keywords: ATP; calmodulin binding; phosphotransferase; protein kinase
 F;38-328/domain: protein kinase homology <KLN>
 F;46-54/region: protein kinase ATP-binding motif

Query Match 63.2%; Score 43; DB 2; Length 377;
 Best Local Similarity 69.2%; Pred. No. 69;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AARASGPGGGAPR 13
 |||||
 Db 1 AAAAPGGGGGEP 13

RESULT 10
 JC1451
 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) - rat
 N;Alternate names: ERK1-MAP kinase; extracellular signal-regulated kinase
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C;Accession: JC1451; A35061; A37140; A40466; S24947
 R;Marquardt, B.; Stabel, S.
 Gene 120, 297-299, 1992
 A;Title: Sequence of a rat cDNA encoding the ERK1-MAP kinase.
 A;Reference number: JC1451; MUID:93013050; PMID:1327976
 A;Accession: JC1451
 A;Molecule type: mRNA
 A;Residues: 1-380 <NAR>
 A;Cross-references: UNIPROT:P21708; UNIPARC:UPI000012F174; EMBL:X65198; NID:G56626; PID:
 A;Experimental source: brain
 R;Boulton, T.G.; Yancopoulos, G.D.; Gregory, J.S.; Slaughter, C.; Moosaw, C.; Hsu, J.;
 Science 249, 64-67, 1990
 A;Title: An insulin-stimulated protein kinase similar to yeast kinases involved in cell
 A;Reference number: A35061; MUID:90312137; PMID:2164259
 A;Accession: A35061
 A;Molecule type: mRNA
 A;Residues: 14-380 <BOU>
 A;Cross-references: UNIPARC:UPI0000145072; GB:M38194; NID:G204051; PIDN:AAA41123.1; PID
 R;Boulton, T.G.; Gregory, J.S.; Cobb, M.H.
 Biochemistry 30, 278-286, 1991
 A;Title: Purification and properties of extracellular signal-regulated kinase 1, an ins
 A;Reference number: A37140; MUID:91105092; PMID:1846291
 A;Accession: A37140
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 43-64;167-178,'X',180-183,'X',185 <BO2>
 A;Cross-references: UNIPARC:UPI000017558F; UNIPARC:UPI0000175590
 R;De Miguel, C.; Kligman, D.; Patel, J.; Detera-Wadleigh, S.D.
 DNA Cell Biol. 10, 505-514, 1991
 A;Title: Molecular analysis of microtubule-associated protein-2 kinase cDNA from mouse
 A;Reference number: A40466; MUID:91369479; PMID:1716439
 A;Accession: A40466
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 14-94,'R',96-380 <DEM>

A:Cross-references: UNIPARC:UPI00001707CE; GB:U12008; GB:S59509; NID:G515498; PIDN:AAA20
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; calmodulin binding; phosphoprotein; phosphotransferase; serine/threonin
F:41-331/Domain: protein kinase homology <KIN>
F:49-57/Region: protein kinase ATP-binding motif

Query Match 63.2%; Score 43; DB 2; Length 380;
Best Local Similarity 69.2%; Pred. No. 70;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AARASPGGGGAPR 13
||| |||||
Db 4 AAAPGGGGGRR 16

RESULT 11

S02165
regulatory protein flay - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C:Accession: S02165
R:Kaplan, J.B.; Dingwall, A.; Bryan, R.; Chamber, R.; Shapiro, L.
J. Mol. Biol. 205, 71-83, 1989

A:Title: Temporal regulation and overlap organization of two Caulobacter flagellar genes
A:Reference number: S02164; MUID:89178645; PMID:2648000
A:Accession: S02165
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-679 <KAP>
A:Cross-references: UNIPROT:PI5345; UNIPARC:UPI000017A8F7
C:Genetics:
A:Gene: flay
C:Keywords: transcription regulation

Query Match 63.2%; Score 43; DB 2; Length 679;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AARASPGGGGAP 12
||| |||||
Db 170 AGTAGGPGGAGAP 181

RESULT 12

A87431
regulatory protein FlayY [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: A87431

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: A87431
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-954 <STO>
A:Cross-references: UNIPROT:PI5345; UNIPARC:UPI000012A8ED; GB:AE005673; NID:G13422833; F

A:Gene: CC1465

Query Match 63.2%; Score 43; DB 2; Length 954;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AARASPGGGAP 12
||| |||||
Db 314 ACTAGGPGGAGAP 325

RESULT 13

H87399
peptidyl-tRNA hydrolase [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: H87399
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: H87399
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-143 <STO>
A:Cross-references: UNIPROT:Q9A9Y3; UNIPARC:UPI00000C72F1; GB:AE005673; NID:G13422540; I

A:Gene: CC1214

Query Match 61.8%; Score 42; DB 2; Length 143;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AARASPGGG 9
||| |||||
Db 22 ATRASPGGG 30

RESULT 14

G72663
hypothetical protein APE0734 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: G72663
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takai
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: G72663
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-201 <KAW>
A:Cross-references: UNIPROT:Q9YE35; UNIPARC:UPI000005DC7C; DDBJ:AF000060; NID:G5104188;

A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0734
C:Superfamily: Aeropyrum pernix hypothetical protein APE0734

Query Match 61.8%; Score 42; DB 2; Length 201;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ARASPGGGGAPR 13
||||| |||||
Db 37 ARASVGGRPR 48

RESULT 15

T29031
hypothetical protein F53G12.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29031
R:Wu, X.; Graves, T.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid F53G12.
A:Reference number: Z20555
A:Accession: T29031
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-327 <WUX>
A:Cross-references: UNIPROT:O01799; UNIPARC:UPI0000078PFF; EMBL:AF003139; PIDN:AA54156

QY 1 AARASPGGGAP 12
||| |||||
Db 314 ACTAGGPGGAGAP 325

A;Experimental source: strain Bristol N2; clone F53G12

C;Genetics:

A;Gene: CESP:F53G12.7

A;Map position: 1

A;Introns: 59/3; 138/1; 223/2

Query Match 61.8%; Score 42; DB 2; Length 327;
Best Local Similarity 72.7%; Pred. No. 85;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ARASGPGGGAP 12

Db 113 AEAAGGGGGAP 123

Search completed: March 13, 2006, 19:16:11

Job time : 16.4471 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 18:53:23 ; Search time 94.3647 Seconds
(without alignments)
97.196 Million cell updates/sec

Title: US-09-529-206E-28
Perfect score: 68
Sequence: 1 AARASGPGGGAPR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	100.0	142	2 Q9NY13 HUMAN	Q9NY13 homo sapien
2	68	100.0	180	1 CTG1B HUMAN	P78358 homo sapien
3	68	100.0	180	2 O7LBY4 HUMAN	O7LBY4 homo sapien
4	60	88.2	210	1 CTAG2 HUMAN	O75638 homo sapien
5	54	79.4	362	2 Q63QT8 BURPS	Q63qt8 burkholderi
6	54	79.4	362	2 Q62H22 BURMA	Q62h22 burkholderi
7	52	76.5	321	2 Q96S27 HUMAN	Q96s27 homo sapien
8	51	75.0	367	2 Q6AV33 ORYSA	Q6av33 oryza sativ
9	50	73.5	194	2 Q96BU2 HUMAN	Q96bu2 homo sapien
10	50	73.5	895	2 Q4NUK4_9DELTA	Q4nuk4 anaeromyxob
11	50	73.5	896	2 Q96D18 HUMAN	Q96d18 homo sapien
12	50	73.5	1253	2 Q6DHV6 HUMAN	Q6dhv6 homo sapien
13	50	73.5	1430	2 Q9H7P9 HUMAN	Q9h7p9 homo sapien
14	49	72.1	175	1 PACA CHICK	P41534 g glucagon-
15	49	72.1	322	2 Q67B70 SYMTH	Q67bj0 symbiobacte
16	49	72.1	788	2 Q4QOP8 HUMAN	Q4qp8 homo sapien
17	48	70.6	159	2 Q63KC9 BURPS	Q63kc9 burkholderi
18	48	70.6	159	2 Q62DA7 BURMA	Q62da7 burkholderi
19	48	70.6	262	2 Q5Z8E2 ORYSA	Q5z8e2 oryza sativ
20	48	70.6	449	2 Q7F1E3 ORYSA	Q7fie3 oryza sativ
21	48	70.6	1133	2 Q4SDN7 TETNG	Q4sdn7 tetraodon n
22	48	70.6	3753	2 Q846W6_STROM	Q846w6 streptomyce
23	47	69.1	108	2 Q8H321 ORYSA	Q8h321 oryza sativ
24	47	69.1	178	2 Q5AF08 CANAL	Q5af08 candida alb
25	47	69.1	702	2 Q4NQW2_9DELTA	Q4ngw2 anaeromyxob
26	46	67.6	327	2 Q63HT9 BURPS	Q63ht9 burkholderi
27	46	67.6	330	2 Q62SN3 BURMA	Q62sn3 burkholderi
28	46	67.6	341	2 Q6H6A6_CRYSA	Q6h6a6 oryza sativ
29	46	67.6	359	2 Q6Z528 ORYSA	Q6z528 oryza sativ
30	46	67.6	383	2 Q4TEG9 TETNG	Q4teg9 tetraodon n
31	46	67.6	398	2 Q8N6H2_HUMAN	Q8n6h2 homo sapien

32 46 67.6 398 2 Q5SQU1 HUMAN
33 46 67.6 399 2 Q8IVQ3 HUMAN
34 46 67.6 425 2 Q4NNI2_9DELTA
35 46 67.6 447 2 Q9GRA8_GRYBI
36 46 67.6 566 2 Q5SQT4 HUMAN
37 46 67.6 644 2 Q688J5 ORYSA
38 46 67.6 684 2 Q51415_PSEAE
39 46 67.6 695 2 Q4T320_TETNG
40 46 67.6 708 2 Q5KJMS_CRYNE
41 46 67.6 708 2 Q5SWM1_CRYNE
42 46 67.6 935 2 Q4P9H9_USTMA
43 46 67.6 1000 2 Q4FKF7_9TRYP
44 45 66.2 309 2 Q63N33_BURPS
45 45 66.2 310 2 Q89JY8_BRAJA

Q5sequ1 homo sapien
Q8ivq3 homo sapien
Q4nni2 anaeromyxob
Q9gra8 gryllus blm
Q5sqt4 homo sapien
Q688j5 oryza sativ
Q51415 pseudomonas
Q4t320 tetraodon n
Q5kjm5 cryptococcu
Q5swm1 cryptococcu
Q4p9h9 ustilago ma
Q4fkf7 trypanosoma
Q63n33 burkholderi
Q89jy8 bradyrhizob

ALIGNMENTS

RESULT 1
Q9NY13 HUMAN
ID Q9NY13_HUMAN PRELIMINARY; PRT; 142 AA.
AC Q9NY13;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Hypothetical protein LAGE-2 (Fragment).
GN Name=LAGE-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ275978; CAB76945.1; -; mRNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;

Query Match 100.0%; Score 68; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AARASGPGGGAPR 13
|||
Db 24 AARASGPGGGAPR 36
|||

RESULT 2
CTG1B HUMAN
ID CTG1B_HUMAN STANDARD; PRT; 180 AA.
AC P78358;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-ESO-1).
GN Name=CTAG1B; Synonyms=CTAG, CTAG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=97203361; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
RA Chen Y.-T., Scanlan M.J., Sahin U., Tuerci O., Gure A.O., Tsang S.,
Williamson B., Stockert E., Pfundschuh M., Old L.J.;
RT "A testicular antigen aberrantly expressed in human cancers detected
by autologous antibody screening.";

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RL Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Melanoma;
RX MEDLINE=98289662; PubMed=9626360;
RA Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA de Plaen E., Boon T.;
RT "LAGE-1, a new gene with tumor specificity.";
RL Int. J. Cancer 76:903-908(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98430682; PubMed=9759882;
RA Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,
RA Schwartztruber D.J., Rosenberg S.A.;
RT "A breast and melanoma-shared tumor antigen: T cell responses to
RT antigenic peptides translated from different open reading frames.";
RL J. Immunol. 161:3596-3606(1998).
CC -!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide
CC variety of cancers. Detected in uterine myometrium.
CC -!- SIMILARITY: Belongs to the CTAG family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U87459; AAB49693.1; -; mRNA.
DR EMBL; AJ003149; CAA05908.1; -; mRNA.
DR EMBL; AF038567; AAD05202.1; -; mRNA.
DR HGNC; HGNC:2491; CTAG1B.
DR MIM; 300156; -.
KW Antigen; Transmembrane.
FT TRANSMEM 156 172 Potential.
FT COMPIAS 5 82 Gly-rich.
SQ SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;

Query Match 100.0%; Score 68; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ct 1 AARASGPGGGAPR 13
Db 50 AARASGPGGGAPR 62

RESULT 3
O7LBV4 HUMAN PRELIMINARY; PRT; 180 AA.
AC O7LBV4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
DE antigen 1-A).
GN Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21303268;
RA Galgoczy P., Rosenthal A., Platzer M.;
RT "Human-mouse comparative sequence analysis of the NEMO gene reveals an
RT alternative promoter within the neighboring G6PD gene.";
RL Gene 271:93-98(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21566154; PubMed=11709543; DOI=10.1093/hmg/10.22.2557;
RA Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
RA Patlan H., Ciccodicola A., Kenwick S., Platzer M., D'Urso M.,
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RA Nelson D.L.;
RT "Multiple pathogenic and benign genomic rearrangements occur at a 35
RT kb duplication involving the NEMO and LAGE2 genes.";
RL Hum. Mol. Genet. 10:2557-2567(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Platzer M.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Platzer M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Galgoczy P., Platzer M.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99454989; PubMed=10523621;
RA De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
RT "DNA methylation is the primary silencing mechanism for a set of germ
RT line- and tumor-specific genes with a CpG-rich promoter.";
RL Mol. Cell. Biol. 19:7327-7335(1999).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF277315; AAL27014.1; -; Genomic DNA.
DR EMBL; AF275977; CAB76943.1; -; Genomic DNA.
DR EMBL; AF277315; AAL27013.1; -; Genomic DNA.
SQ SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;

Query Match 100.0%; Score 68; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ct 1 AARASGPGGGAPR 13
Db 50 AARASGPGGGAPR 62

RESULT 4
CTAG2 HUMAN STANDARD; PRT; 210 AA.
AC O75638; O75637; Q9BU80; Q9UJ89; Q9Y479;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
GN Name=CTAG2; Synonyms=ESO2, LAGE1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B).
RC TISSUE=Melanoma;
RX MEDLINE=98289662; PubMed=9626360;
RA Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA de Plaen E., Boon T.;
RT "LAGE-1, a new gene with tumor specificity.";
RL Int. J. Cancer 76:903-908(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B), AND VARIANTS
RP GLN-6; GLN-89 AND ARG-138.
RC TISSUE=Melanoma;
RX MEDLINE=99325550; PubMed=10399963;
RA Arnouldse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT unexpected translation product of LAGE-1.";
RL Int. J. Cancer 82:442-448(1999).
RN [3]
```

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-1B), AND VARIANT
RP ARG-138.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Names=LAGE-1B; Synonyms=LAGE-1L;
CC IsoId=O75638-1; Sequence=Displayed;
CC Names=LAGE-1A; Synonyms=LAGE-1S;
CC IsoId=O75638-2; Sequence=VSP_004301;
CC -!- TISSUE SPECIFICITY: Testis and very low level in placenta and in
CC some uterus samples. Observed in 25-50% of tumor samples of
CC melanomas, non-small-cell lung carcinomas, bladder, prostate and
CC head and neck cancers.
CC -!- DOMAIN: A transmembrane domain is present in isoform LAGE-1A.
CC -!- SIMILARITY: Belongs to the CPAG family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AJ223093; CAAL1111.1; -; Genomic DNA.
CC EMBL; AJ223093; CAAL1116.1; -; Genomic DNA.
DR EMBL; AJ223040; CAAL1043.1; -; mRNA.
DR EMBL; AJ223041; CAAL1044.1; -; mRNA.
DR EMBL; AJ012834; CAAL0194.1; -; mRNA.
DR EMBL; AJ012835; CAAL0196.1; -; mRNA.
DR EMBL; BC002833; AAH02833.1; -; mRNA.
DR Ensembl; ENSG00000126890; Homo sapiens.
DR HGNC; HGNC:2492; CPAG2.
DR H-InvDB; HIX0017163; -.
DR MIM; 300396; -.
KW Alternative splicing; Antigen; Polymorphism; Transmembrane.
FT COMPBIAS 5 79 Gly-rich.
FT COMPBIAS 183 188 Poly-Pro.
FT VARSPLIC 135 210 MSVNDQREAGRMVRVVGWGLGSGASPEGQKARDLRTPKHKV
FT SEQRRPGPPGPPGAGQDGCRCGVAENVMSAPHI -> IR
FT LTRADHRQLQSISCLQLSLMLWITQCFLPVLQAQPSG
FT QRR (in isoform LAGE-1A).
FT /FTid=VSP_004301.
FT R -> Q.
FT /FTid=VAR_007855.
FT E -> Q.
FT /FTid=VAR_007856.
FT W -> R.
FT /FTid=VAR_007857.
FT /FTid=VAR_007857.
SQ SEQUENCE 210 AA; 21120 MW; 9BE0E0A855E8BE CRC64;

Query Match 88.2%; Score 60; DB 1; Length 210;
Best Local Similarity 92.3%; Pred. No. 1.1;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AARASGPGGAPR 13
DB 50 AARASGPGGAPR 62
|||||
RESULT 5
Q63Q78_BURPS PRELIMINARY; PRT; 362 AA.
ID Q63Q78_BURPS
AC Q63Q78; 28-0CT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Putative DNA polymerase III.
GN OrderedLocusNames=BPSI2936;
OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; pseudomallei group.
OX NCBI_TaxID=28450;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K96243;
RX PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosssett B., Davis P., Deshazer D.,
RA Feitwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinovitch E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilai S., Stevens K., Tumapa S., Vesaratchaveat M.,
RA Whitehead S., Yeates C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).
DR EMBL; BX571965; CAH36946.1; -; Genomic DNA.
DR GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR GO; GO:0006260; P:DNA replication; IEA.
DR InterPro; IPR010372; DNA_polIII_delta.
DR InterPro; IPR005790; DNA_polIII_delta.
DR Pfam; PF06144; DNA_pol3_delta; 1.
DR TIGRFAMs; TIGR01128; hoIA; 1.
KW Complete proteome.
SQ SEQUENCE 362 AA; 38726 MW; D5FF3DE783D41E41 CRC64;

Query Match 79.4%; Score 54; DB 2; Length 362;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AARASGPGGAPR 13
DB 348 AARASGPGDAPR 359
|||||
RESULT 6
Q62H22_BURMA PRELIMINARY; PRT; 362 AA.
ID Q62H22_BURMA
AC Q62H22;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE DNA polymerase III, delta subunit (EC 2.7.7.7).
GN Name=hoIA; OrderedLocusNames=BMA2451;
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=13373;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 23344;
RX PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,

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RA Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA Daugherty S.C., Davidson T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
RA Sarria S., Sengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA Zafar N., Zhou L., Fraser C.M.,
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251 (2004).
DR EMBL; CP000010; AAU49707.1; -; Genomic_DNA.
DR TIGR; BMA2451; -.
DR GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008260; P:DNA replication; IEA.
DR InterPro; IPR010372; DNA_pol3_delta.
DR InterPro; IPR005790; DNA_pol3_delta.
DR Pfam; PF06144; DNA_pol3_delta; 1.
DR TIGRFAMs; TIGR01128; hofA; 1.
KW Complete proteome; Nucleotidyltransferase; Transferase.
SQ SEQUENCE 362 AA; 38726 MW; D5FP3DE783D41E41 CRC64;

Query Match 79.4%; Score 54; DB 2; Length 362;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARASGPGGGAPR 13
DB 348 ARAAGPGGDAPR 359
|||||
RESULT 7
Q96S27 HUMAN
ID Q96S27_HUMAN PRELIMINARY; PRT; 321 AA.
AC Q96S27;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein gene X.
GN Name=gene X;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21096910; PubMed=11157797; DOI=10.1093/hmg/10.4.339;
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA Higgs D.R.;
RT "Sequence, structure and pathology of the fully annotated terminal 2
RT Mb of the short arm of human chromosome 16.";
RL Hum. Mol. Genet. 10:339-352(2001).
DR EMBL; AB006463; AAK61225.1; -; Genomic DNA.
DR Ensembl; ENSG00000167933; Homo sapiens.
KW Hypothetical protein.
SQ SEQUENCE 321 AA; 32979 MW; 9C8764CFA17F4CD4 CRC64;

Query Match 76.5%; Score 52; DB 2; Length 321;
Best Local Similarity 76.9%; Pred. No. 22;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 13
DB 5 AARRAGPGGGAPR 17
|||||
RESULT 8
Q6AV33 ORYSA
ID Q6AV33_ORYSA PRELIMINARY; PRT; 367 AA.
AC Q6AV33;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

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DE Hypothetical protein OSJNBa0063J18.9.
GN Name=OSJNBa0063J18.9;
OC Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA Vanaken S., Riedmuller S.B., Uterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSJNBa0063J18 genomic sequence.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC107206; AAT77052.1; -; Genomic DNA.
DR Gramene; O6AV33; -.
KW Hypothetical protein.
SQ SEQUENCE 367 AA; 37474 MW; B8C62D9D4CC18C86 CRC64;

Query Match 75.0%; Score 51; DB 2; Length 367;
Best Local Similarity 76.9%; Pred. No. 35;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AARASGPGGGAPR 13
DB 91 AARASGPGGGAR 103
|||||
RESULT 9
Q96BU2 HUMAN
ID Q96BU2_HUMAN PRELIMINARY; PRT; 194 AA.
AC Q96BU2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PLEKHG2 protein (Fragment).
GN Name=PLEKHG2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Pancreas;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

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RN RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pancreas;
RA Director MGC Project;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015174; AAL15174.1; -; mRNA.
FT NON_TER
SQ SEQUENCE 194 AA; 19957 MW; 91AB4FF8F05CDB3C CRC64;

Query Match 73.5%; Score 50; DB 2; Length 194;
Best Local Similarity 81.8%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ARASGPGGGAP 12
Db 99 ARRQGGGGAP 109

RESULT 10
Q4NUK4_9DELTA PRELIMINARY; PRT; 895 AA.
AC Q4NUK4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE L1gA.
GN ORFNames=AdehDRAFT 2813;
OS Anaeromyxobacter dehalogenans 2CP-C.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
OX NCBI_TaxID=290397;
RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-PCF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Anaeromyxobacter
RT dehalogenans 2CP-C.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT Annotation of the draft genome assembly of Anaeromyxobacter
RT dehalogenans 2CP-C.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHD0100013; EAL79351.1; -; Genomic DNA.
SQ SEQUENCE 895 AA; 93871 MW; 0AE25BBBF172BD80 CRC64;

Query Match 73.5%; Score 50; DB 2; Length 895;
Best Local Similarity 76.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AARASGPGGGAPR 13
Db 797 ARBARGAGGGAPR 809

RESULT 11
Q96D18_HUMAN
ID Q96D18_HUMAN PRELIMINARY; PRT; 896 AA.
AC Q96D18;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PLEKHG2 protein.
GN Name=PLEKHG2;
OS Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
Homo.
NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Pancreas;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Pancreas;
RA Director MGC Project;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013426; AAH13426.1; -; mRNA.
SQ SEQUENCE 896 AA; 94247 MW; 0DE6869BCFD4C471 CRC64;

Query Match 73.5%; Score 50; DB 2; Length 896;
Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ARASGPGGGAP 12
Db 801 ARRQGGGGAP 811

RESULT 12
Q6DHV6_HUMAN
ID Q6DHV6_HUMAN PRELIMINARY; PRT; 1253 AA.
AC Q6DHV6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE PLEKHG2 protein (Fragment).
GN Name=PLEKHG2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Pancreas;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton B., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
EA Butterfield Y.S.N., Krzywinski M.I., Skaleja U., Smailus D.E.,
EA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
EL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pancreas;
RA Director MGC Project;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 PH domain.
DR EMBL; BC075858; AAH75858.1; -; mRNA.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhoGEF.
DR Pfam; PF00169; PH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR PROSITE; PS50010; DH 2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
FT NON_TER 1
SQ SEQUENCE 1253 AA; 134404 MW; 534EB31283E535C5 CRC64;

Query Match 73.5%; Score 50; DB 2; Length 1253;
Best Local Similarity 81.8%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ARASGPGGGAP 12
DB 1158 ARROGPGGGAP 1168

RESULT 13
Q9H7P9 HUMAN
ID Q9H7P9 HUMAN PRELIMINARY; PRT; 1430 AA.
AC Q9H7P9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE FLJ00018 protein (fragment).
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX PubMed=14702039; DOI=10.1038/ngl1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Oobayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimachi S., Watanabe M., Hirooka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fuji A., Hara H., Tanase T.-O.,
RA Nomura Y., Togliya S., Komai F., Hara K., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama N., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

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RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Maekumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45 (2004).
CC -!- SIMILARITY: Contains 1 PH domain.
DR EMBL; AK024429; BAB15719.1; -; mRNA.
DR HSSP; Q64096; 1KZ7.
DR HGNC; HGNC:29515; PLEKHG2.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhoGEF.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhoGEF; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR PROSITE; PS50010; DH 2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
FT NON_TER 1
SQ SEQUENCE 1430 AA; 152528 MW; E4DF0BFDAACCB6A30 CRC64;

Query Match 73.5%; Score 50; DB 2; Length 1430;
Best Local Similarity 81.8%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ARASGPGGGAP 12
DB 1335 ARROGPGGGAP 1345

RESULT 14
PACA_CHICK
ID PACA_CHICK STANDARD; PRT; 175 AA.
AC P41534; O53WVO;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Glucagon-family neuropeptides precursor [Contains: Growth hormone-
DE releasing factor 1-46 (GRF) (Growth hormone-releasing hormone) (GHRH);
DE pituitary adenylate cyclase activating polypeptide-27 (PACAP-27)
DE (PACAP27); Pituitary adenylate cyclase activating polypeptide-38
DE (PACAP-38) (PACAP38)].
GN Name=ADCYAP1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA / mRNA].
RX MEDLINE=97174314; PubMed=9022048;
RA McRory J.E., Parker R.L., Sherwood N.M.;
RT "Expression and alternative processing of a chicken gene encoding both
RT growth hormone-releasing hormone and pituitary adenylate cyclase-
RT activating polypeptide."
RL DNA Cell Biol. 16:95-102 (1997).
RN [2]
RP PROTEIN SEQUENCE OF 131-168.
RA Yasuhara T., Mizuno K., Somogyvari-Vigh A., Komaki G., Arimura A.;
RT "Isolation and primary structure of chicken PACAP."
RL Regul. Pept. 37:326-326 (1992).
CC -!- FUNCTION: Primary role of GRF is to release GH from the pituitary.
CC -!- FUNCTION: PACAP plays pivotal roles as a neurotransmitter and/or a
CC neuromodulator.
CC -!- SUBCELLULAR LOCATION: Secreted.

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CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=GRF 1-46;
CC IsoId=P41534-1; Sequence=Displayed;
CC Name=GRF 1-43;
CC IsoId=P41534-2; Sequence=VSP_001760;
CC Name=GRF 33-46;
CC IsoId=P41534-3; Sequence=VSP_001759;
CC -!- SIMILARITY: Belongs to the glucagon family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U71183; AAB51200.1; -; mRNA.
CC EMBL; U71184; AAB51201.1; -; mRNA.
CC EMBL; U71185; AAB51202.1; -; mRNA.
CC EMBL; U67275; AAC64494.1; -; Genomic_DNA.
CC HSP; P18509; IGCA.
CC InterPro: IPR000532; Glucagon.
CC Pfam; PF00123; Hormone_2; 2.
CC PRINTS; PR00275; GLUCAGON.
CC PROSITE; PS00260; GLUCAGON; 2.
CC KW Alternative splicing; Amidation; Cleavage on pair of basic residues;
CC Direct protein sequencing; Glucagon family; Hormone; Signal.
CC FT SIGNAL 1 23 Potential.
CC FT PROPEP 24 80
CC FT PEPTIDE 83 128
CC FT PEPTIDE 131 168
CC FT PEPTIDE 131 157
CC FT PROPEP 172 175
CC FT MOD_RES 157 157
CC FT MOD_RES 168 168
CC FT VARSPLIC 82 114
CC FT VARSPLIC 115 117
CC FT SEQUENCE 175 AA; 19561 MW; 0DB54995F0AA9DFB CRC64;
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CC Query Match 72.1%; Score 49; DB 1; Length 175;
CC Best Local Similarity 69.2%; Pred. No. 33;
CC Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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CC QY 1 AARASGPGGAPR 13
CC DB 54 ALRAGPGGGPR 66
CC
CC RESULT 15
CC Q67PJ0_SYNTH
CC ID Q67PJ0_SYNTH PRELIMINARY; PRT; 322 AA.
CC AC Q67PJ0;
CC DT 25-OCT-2004 (TrEMBLrel. 28, Created)
CC DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
CC DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
CC DE Prephenate dehydrogenase.
CC GN OrderedLocNames=StrH418;
CC OS Symbiobacterium thermophilum.
CC OC Bacteria; Actinobacteria; Symbiobacterium.
CC OX NCBI_TaxID=2734;
CC RN [1]
CC RP NUCLEOTIDE SEQUENCE.
CC RC STRAIN=IAM14863;
CC RX PubMed=15383646; DOI=10.1093/nar/gkh830;
CC RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsui T.,
CC Morimura K., Ikeda H., Hattori M., Beppu T.;
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RT "Genome sequence of Symbiobacterium thermophilum, an uncultivable
RL bacterium that depends on microbial commensalism.";
RL Nucleic Acids Res. 32:4937-4944(2004).
DR EMBL; AP006840; BAD40403.1; -; Genomic DNA.
DR GO; GO:0004665; F:prephenate dehydrogenase (NADP+) activity; IEA.
DR GO; GO:0006571; P:tyrosine biosynthesis; IEA.
DR InterPro; IPR003099; Prephen_dehydrog.
DR Pfam; PF02153; PDH; 1.
DR KW Complete proteome.
DR SQ SEQUENCE 322 AA; 32843 MW; 09A06AC0AFA734EC CRC64;
CC
CC Query Match 72.1%; Score 49; DB 2; Length 322;
CC Best Local Similarity 90.9%; Pred. No. 58;
CC Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC
CC QY 1 AARASGPGGGA 11
CC DB 45 AADASGPGGGA 55
CC
CC Search completed: March 13, 2006, 19:14:27
CC Job time : 94.3647 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:14:49 ; Search time 24.1647 Seconds
(without alignments)
44.477 Million cell updates/sec

Title: US-09-529-206E-28
Perfect score: 68
Sequence: 1 AARASGPGGAPR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/6 COMB.pap:*
3: /cgn2_6/ptodata/1/iaa/H COMB.pap:*
4: /cgn2_6/ptodata/1/iaa/PTUS COMB.pap:*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pap:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	100.0	180	1	US-08-791-495-9
2	68	100.0	180	2	US-08-937-263B-8
3	68	100.0	180	2	US-09-751-798-8
4	68	100.0	180	2	US-09-392-714-25
5	68	100.0	180	2	US-09-165-546D-15
6	68	100.0	180	2	US-09-341-829A-9
7	68	100.0	180	2	US-09-849-602-30
8	60	88.2	180	1	US-08-791-495-7
9	60	88.2	180	2	US-09-341-829A-7
10	60	88.2	210	1	US-08-791-495-5
11	50	88.2	210	2	US-09-341-829A-5
12	50	73.5	160	2	US-09-252-991A-17249
13	49	72.1	143	2	US-08-789-329C-10
14	49	72.1	172	2	US-08-789-329C-7
15	49	72.1	175	2	US-08-789-329C-3
16	49	72.1	416	2	US-09-252-991A-30219
17	48	70.6	9	2	US-09-344-040C-117
18	48	70.6	9	2	US-09-833-039A-117
19	48	70.6	196	2	US-09-252-991A-30527
20	48	70.6	421	2	US-09-252-991A-32326
21	48	70.6	456	2	US-09-252-991A-17335
22	48	70.6	809	2	US-09-252-991A-17359
23	48	70.6	1427	2	US-09-252-991A-20577
24	46	67.6	210	2	US-09-252-991A-24923
25	46	67.6	789	2	US-09-252-991A-25611
26	45	66.2	187	2	US-09-252-991A-29442
27	45	66.2	678	2	US-10-104-047-3295

28	45	66.2	679	2	US-09-252-991A-27111	Sequence 27111, A
29	45	66.2	727	2	US-09-902-540-12383	Sequence 12383, A
30	44	64.7	186	2	US-09-252-991A-16943	Sequence 16943, A
31	44	64.7	242	2	US-08-220-602B-23	Sequence 23, Appl
32	44	64.7	242	2	US-09-861-012A-23	Sequence 23, Appl
33	44	64.7	242	2	US-09-861-098A-23	Sequence 23, Appl
34	44	64.7	242	2	US-09-861-097-23	Sequence 23, Appl
35	44	64.7	357	2	US-09-252-991A-28380	Sequence 28380, A
36	44	64.7	379	2	US-08-622-277A-8	Sequence 8, Appl
37	44	64.7	379	2	US-09-025-580-25	Sequence 25, Appl
38	44	64.7	379	2	US-09-411-628-14	Sequence 14, Appl
39	44	64.7	379	2	US-10-174-794-14	Sequence 14, Appl
40	44	64.7	379	2	US-09-538-092-1021	Sequence 1021, Ap
41	44	64.7	379	2	US-09-642-749-25	Sequence 25, Appl
42	44	64.7	631	2	US-09-417-197-39	Sequence 39, Appl
43	44	64.7	974	2	US-08-938-291A-4	Sequence 4, Appl
44	44	64.7	974	2	US-09-589-619-4	Sequence 4, Appl
45	43	63.2	165	2	US-09-270-767-59895	Sequence 59895, A

ALIGNMENTS

RESULT 1
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 68; DB 1; Length 180;

Best Local Similarity 100.0%; Pred. No. 0.068; 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0;

QY 1 AARASGPGGAPR 13

|||||

Db 50 AARASGPGGAPR 62

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RESULT 2
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tsang; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-08-937-263B-8
;
; Query Match 100.0%; Score 68; DB 2; Length 180;
; Best Local Similarity 100.0%; Pred. No. 0.068;
; Mismatches 0; Indels 0; Gaps 0;
; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AARASPGGGAPR 13
Db 50 AARASPGGGAPR 62

RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tsang; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
```

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; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6525177man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-09-751-798-8
;
; Query Match 100.0%; Score 68; DB 2; Length 180;
; Best Local Similarity 100.0%; Pred. No. 0.068;
; Mismatches 0; Indels 0; Gaps 0;
; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AARASPGGGAPR 13
Db 50 AARASPGGGAPR 62

RESULT 4
US-09-392-714-25
; Sequence 25, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tsang
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-392-714-25
;
; Query Match 100.0%; Score 68; DB 2; Length 180;
; Best Local Similarity 100.0%; Pred. No. 0.068;
; Mismatches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AARASPGGGAPR 13
Db 50 AARASPGGGAPR 62
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RESULT 5
US-09-165-546D-15
; Sequence 15, Application US/09165546D
; Patent No. 6723832
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
;       Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;       SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
;       USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546D
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6723832man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15

Query Match      100.0%; Score 68; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AARASGPGGGAPR 13
      |||||
DB      50 AARASGPGGGAPR 62

RESULT 6
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
<151> 1997-01-27

US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30

Query Match      100.0%; Score 68; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AARASGPGGGAPR 13
      |||||
DB      50 AARASGPGGGAPR 62

RESULT 7
US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30

Query Match      100.0%; Score 68; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AARASGPGGGAPR 13
      |||||
DB      50 AARASGPGGGAPR 62

RESULT 8
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth , Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-7

Query Match      88.2%; Score 60; DB 1; Length 180;
Best Local Similarity 92.3%; Pred. No. 0.75;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AARASGPGGGAPR 13
      ||||| |||||
Db      50 AARASGPRGGAPR 62

RESULT 9
US-09-341-829A-7
; Sequence 7, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-7

Query Match      88.2%; Score 60; DB 2; Length 180;
Best Local Similarity 92.3%; Pred. No. 0.75;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AARASGPGGGAPR 13
      ||||| |||||
Db      50 AARASGPRGGAPR 62

RESULT 10
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

; APPLICATION NUMBER: US/08/791,495
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-5

Query Match      88.2%; Score 60; DB 1; Length 210;
Best Local Similarity 92.3%; Pred. No. 0.86;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AARASGPGGGAPR 13
      ||||| |||||
Db      50 AARASGPRGGAPR 62

RESULT 11
US-09-341-829A-5
; Sequence 5, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-5

Query Match      88.2%; Score 60; DB 2; Length 210;
Best Local Similarity 92.3%; Pred. No. 0.86;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AARASGPGGGAPR 13
      ||||| |||||
Db      50 AARASGPRGGAPR 62

RESULT 12
```

US-09-252-991A-17249
; Sequence 17249, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17249
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17249

Query Match 73.5%; Score 50; DB 2; Length 160;
Best Local Similarity 69.2%; Pred. No. 13;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AARASGPGGGAPR 13
| | | | | | | | | |
DB 117 AGRAGEGGSAPR 129

RESULT 13
US-08-789-329C-10
; Sequence 10, Application US/08789329C
; Patent No. 6165755
; GENERAL INFORMATION:
; APPLICANT: SHERWOOD ET AL.
; TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/08/789,329C
; PRIOR FILING DATE: 01/23/97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Eard, David J.
; REGISTRATION NUMBER: 41,401
; REFERENCE/DOCKET NUMBER: 2847-46468/DJE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 143 aa
; TYPE: amino acid
; STRANDEDNESS: single

; TOPOLOGY: linear
US-08-789-329C-10
Query Match 72.1%; Score 49; DB 2; Length 143;
Best Local Similarity 69.2%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 AARASGPGGGAPR 13
| | | | | | | | | |
DB 54 ALRAGAPGGGPR 66
RESULT 14
US-08-789-329C-7
; Sequence 7, Application US/08789329C
; Patent No. 6165755
; GENERAL INFORMATION:
; APPLICANT: SHERWOOD ET AL.
; TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/08/789,329C
; PRIOR FILING DATE: 01/23/97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Eard, David J.
; REGISTRATION NUMBER: 41,401
; REFERENCE/DOCKET NUMBER: 2847-46468/DJE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 172 aa
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-789-329C-7
Query Match 72.1%; Score 49; DB 2; Length 172;
Best Local Similarity 69.2%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 AARASGPGGGAPR 13
| | | | | | | | | |
DB 54 ALRAGAPGGGPR 66
RESULT 15
US-08-789-329C-3
; Sequence 3, Application US/08789329C
; Patent No. 6165755
; GENERAL INFORMATION:
; APPLICANT: SHERWOOD ET AL.

;; TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL
;; TITLE OF INVENTION: FOR IMPROVED POULTRY PRODUCTION
;; NUMBER OF SEQUENCES: 20
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
;; ADDRESSEE: Whinston, LLP
;; STREET: One World Trade Center
;; STREET: 121 S.W. Salmon Street
;; STREET: Suite 1600
;; CITY: Portland
;; STATE: Oregon
;; COUNTRY: United States of America
;; ZIP: 97204-2988
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Disk, 3-1/2 inch
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: Windows NT
;; SOFTWARE: WordPerfect 7.0 & ASCII
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/789,329C
;; FILING DATE: 01/23/97
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Earp, David J.
;; REGISTRATION NUMBER: 41,401
;; REFERENCE/DOCKET NUMBER: 2847-46468/DJE
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (503) 226-7391
;; TELEFAX: (503) 228-9446
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 175 aa
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-789-329C-3

Query Match 72.1%; Score 49; DB 2; Length 175;
Best Local Similarity 69.2%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AARAGPGGGAPR 13
| | | | |
Db 54 ALRAGAPGGGPR 66

Search completed: March 13, 2006, 19:18:51
Job time : 24.1647 secs

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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:51:56 ; Search time 78.6118 Seconds
(without alignments)
69.096 Million cell updates/sec

Title: US-09-529-206E-28
Perfect score: 68
Sequence: 1 AARASGPGGGAPR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	100.0	30	4	US-10-296-734-1404
2	68	100.0	179	5	US-10-482-029-202
3	68	100.0	180	3	US-09-751-798-8
4	68	100.0	180	3	US-09-849-602-30
5	68	100.0	180	4	US-10-023-182-8
6	68	100.0	180	4	US-10-207-655-71
7	68	100.0	180	4	US-10-364-614-14
8	68	100.0	180	4	US-10-026-066-3
9	68	100.0	180	4	US-10-117-937-74
10	68	100.0	180	4	US-10-295-027-386
11	68	100.0	180	4	US-10-296-734-832
12	68	100.0	180	4	US-10-188-832-139
13	68	100.0	180	4	US-10-777-053-11
14	68	100.0	180	4	US-10-751-088-15
15	68	100.0	180	4	US-10-657-022-74
16	68	100.0	180	4	US-10-837-217-11
17	68	100.0	180	5	US-10-877-373-9
18	68	100.0	180	5	US-10-723-860-1270
19	68	100.0	180	5	US-10-871-708-7
20	68	100.0	180	5	US-10-895-523-3
21	68	100.0	180	5	US-10-182-506A-3
22	68	100.0	180	5	US-10-756-149-5024
23	68	100.0	180	6	US-11-067-064-74
24	68	100.0	180	3	US-09-821-883-27
25	68	100.0	397	3	US-11-144-912-27
26	68	100.0	397	6	US-11-144-912-27
27	68	100.0	3541	4	US-10-296-734-1454

28	60	88.2	30	4	US-10-296-734-1436	Sequence 1436, Ap
29	60	88.2	135	4	US-10-295-027-388	Sequence 388, App
30	60	88.2	135	4	US-10-188-832-141	Sequence 141, App
31	60	88.2	180	4	US-10-146-473-69	Sequence 69, Appl
32	60	88.2	180	4	US-10-117-937-75	Sequence 75, Appl
33	60	88.2	180	4	US-10-296-734-834	Sequence 834, App
34	60	88.2	180	4	US-10-468-406-4	Sequence 4, Appli
35	60	88.2	180	4	US-10-657-022-75	Sequence 75, Appli
36	60	88.2	180	5	US-10-877-373-7	Sequence 7, Appli
37	60	88.2	180	6	US-11-067-064-75	Sequence 75, Appl
38	60	88.2	180	6	US-11-067-159-75	Sequence 75, Appl
39	60	88.2	210	4	US-10-157-031-88	Sequence 88, Appl
40	60	88.2	210	4	US-10-117-937-76	Sequence 76, Appl
41	60	88.2	210	4	US-10-657-022-76	Sequence 76, Appl
42	60	88.2	210	5	US-10-877-373-5	Sequence 5, Appli
43	60	88.2	210	6	US-11-067-064-76	Sequence 76, Appl
44	60	88.2	210	6	US-11-067-159-76	Sequence 76, Appl
45	56	82.4	20	4	US-10-313-986-496	Sequence 496, App

ALIGNMENTS

RESULT 1
US-10-296-734-1404
; Sequence 1404, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1404
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA segment 4
US-10-296-734-1404

Query Match 100.0%; Score 68; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AARASGPGGGAPR 13
Db 7 AARASGPGGGAPR 19

RESULT 2
US-10-482-029-202
; Sequence 202, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-202

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Best Local Similarity 100.0%; Pred. No. 0.37; 0; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AARASGPGGGAPR 13
DB      50 AARASGPGGGAPR 62
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RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. US20020010321A1
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. US20020010321A1man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-09-751-798-8

Query Match          100.0%; Score 68; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.37; 0; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AARASGPGGGAPR 13
DB      50 AARASGPGGGAPR 62
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RESULT 4
US-09-849-602-30
; Sequence 30, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
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Query Match          100.0%; Score 68; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AARASGPGGGAPR 13
Db 50 AARASGPGGGAPR 62

RESULT 6
US-10-067-655-71
; Sequence 71, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-655-71

Query Match          100.0%; Score 68; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AARASGPGGGAPR 13
Db 50 AARASGPGGGAPR 62

RESULT 7
US-10-364-614-14
; Sequence 14, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
; APPLICANT: JAGER, Elke
; APPLICANT: KNUTH, Alexander
; APPLICANT: OLD, Lloyd
; APPLICANT: Grjatic, Sacha
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
; FILE REFERENCE: LUD 5726.1 CIP
; CURRENT APPLICATION NUMBER: US/10/364,614
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/355,828
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-614-14

Query Match          100.0%; Score 68; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AARASGPGGGAPR 13
Db 50 AARASGPGGGAPR 62

RESULT 8
US-10-026-066-3
; Sequence 3, Application US/10026066
; Publication No. US20030215425A1
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; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPIOTOPE SYNCHRONIZATION IN ANTIGEN
; TITLE OF INVENTION: PRESENTING CELLS
; FILE REFERENCE: CTLM.21CPC
; CURRENT APPLICATION NUMBER: US/10/026,066
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-026-066-3

Query Match          100.0%; Score 68; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AARASGPGGGAPR 13
Db 50 AARASGPGGGAPR 62

RESULT 9
US-10-117-937-74
; Sequence 74, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J. L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPIOTOPE SEQUENCES
; FILE REFERENCE: CTLM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-74

Query Match          100.0%; Score 68; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AARASGPGGGAPR 13
Db 50 AARASGPGGGAPR 62

RESULT 10
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US-10-295-027-386
; Sequence 386, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 386
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-386

Query Match          100.0%; Score 68; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AARASGPGGGAPR 13
Db      50 AARASGPGGGAPR 62

RESULT 11
US-10-296-734-832
; Sequence 832, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 832

US-10-295-027-386
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYN501a consensus polypeptide
US-10-296-734-832

Query Match          100.0%; Score 68; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AARASGPGGGAPR 13
Db      50 AARASGPGGGAPR 62

RESULT 12
US-10-188-832-139
; Sequence 139, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-139

Query Match          100.0%; Score 68; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AARASGPGGGAPR 13
Db      50 AARASGPGGGAPR 62

RESULT 13
US-10-777-053-11
; Sequence 11, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: MANKK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
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; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-777-053-11

Query Match      100.0%; Score 68; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AARASGPGGAPR 13
Db      50 AARASGPGGAPR 62

RESULT 14
US-10-751-088-15
; Sequence 15, Application US/10751088
; Publication No. US2004015804A1
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
; USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/751,088
; FILING DATE: 02-Jan-2004
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546D
; FILING DATE: 02-Oct-1998
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-10-751-088-15

Query Match      100.0%; Score 68; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 AARASGPGGAPR 13
Db      50 AARASGPGGAPR 62

RESULT 15
US-10-657-022-74
; Sequence 74, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANNK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-657-022-74

Query Match      100.0%; Score 68; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AARASGPGGAPR 13
Db      50 AARASGPGGAPR 62

Search completed: March 13, 2006, 20:02:27
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:54:06 ; Search time 8.87059 Seconds
(without alignments)
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Title: US-09-529-206E-28
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	180	7	US-11-155-288-7
2	68	100.0	240	7	US-11-021-441-28
3	56	82.4	20	6	US-10-623-155-496
4	47	69.1	306	7	US-11-096-568A-20556
5	47	69.1	353	7	US-11-096-568A-22334
6	47	69.1	358	7	US-11-096-568A-22333
7	47	69.1	420	7	US-11-096-568A-22332
8	46	67.6	134	7	US-11-096-568A-23806
9	45	66.2	678	7	US-11-072-512-3295
10	44	64.7	379	7	US-11-109-156-16
11	44	64.7	558	7	US-11-096-568A-26217
12	44	64.7	974	6	US-10-531-036-35
13	43	63.2	413	7	US-11-096-568A-27265
14	42	61.8	162	7	US-11-096-568A-641
15	42	61.8	249	7	US-11-096-568A-23045
16	41.5	61.0	167	7	US-11-096-568A-10542
17	41	60.3	119	7	US-11-110-424-4
18	41	60.3	268	7	US-11-087-099-6009
19	41	60.3	306	7	US-11-100-640-26
20	41	60.3	365	7	US-11-108-528-58
21	41	60.3	537	7	US-11-179-958A-2
22	41	60.3	555	7	US-11-072-512-3369
23	41	60.3	953	7	US-11-037-243-66
24	40.5	59.6	280	7	US-11-143-980-34
25	40	58.8	291	7	US-11-087-099-3763

26	40	58.8	1832	7	US-11-087-099-7762	Sequence 7762, Ap
27	39	57.4	178	7	US-11-096-568A-20715	Sequence 20715, A
28	39	57.4	213	7	US-11-072-512-2722	Sequence 2722, Ap
29	39	57.4	228	7	US-11-096-568A-22508	Sequence 22508, A
30	39	57.4	233	7	US-11-240-769-58	Sequence 58, Appl
31	39	57.4	284	7	US-11-096-568A-11286	Sequence 11286, A
32	39	57.4	298	6	US-10-821-234-1240	Sequence 1240, Ap
33	39	57.4	430	6	US-10-992-577-8	Sequence 8, Appl
34	39	57.4	430	6	US-10-508-892-2	Sequence 2, Appl
35	39	57.4	430	7	US-11-223-294-54	Sequence 54, Appl
36	39	57.4	461	7	US-11-096-568A-18223	Sequence 18223, A
37	39	57.4	493	7	US-11-096-568A-18222	Sequence 18222, A
38	39	57.4	496	7	US-11-096-568A-18221	Sequence 18221, A
39	39	57.4	618	7	US-11-078-735-18	Sequence 18, Appl
40	39	57.4	618	7	US-11-050-346-63	Sequence 63, Appl
41	39	57.4	618	7	US-11-103-077-18	Sequence 18, Appl
42	39	57.4	662	7	US-11-072-175-184	Sequence 184, Appl
43	39	57.4	736	7	US-11-078-189-11	Sequence 11, Appl
44	39	57.4	830	6	US-10-921-793-38	Sequence 38, Appl
45	39	57.4	830	6	US-10-931-198-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-11-155-288-7
; Sequence 7, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; FILE REFERENCE: MANNK.050A
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-7

Query Match 100.0%; Score 68; DB 7; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.011; 0; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AARASGPGGAPR 13
DB 50 AARASGPGGAPR 62

RESULT 2

US-11-021-441-28
; Sequence 28, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; FILE REFERENCE: 282172003900
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US/11/021,441
; PRIOR FILING DATE: 2004-10-06

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; PRIOR APPLICATION NUMBER: US 60/615,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein
US-11-021-441-28
```

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Query Match 100.0%; Score 68; DB 7; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 AARASGPGGGAPR 13
Db 110 AARASGPGGGAPR 122
|||||
```

RESULT 3

```
US-10-623-155-496
; Sequence 496, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 496
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-496
```

```
Query Match 82.4%; Score 56; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AARASGPGGGA 11
Db 10 AARASGPGGGA 20
|||||
```

RESULT 4

```
US-11-096-568A-20556
; Sequence 20556, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20556
```

```
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(306)
; OTHER INFORMATION: Ceres Seq. ID no. 12383286
US-11-096-568A-20556
```

```
Query Match 69.1%; Score 47; DB 7; Length 306;
Best Local Similarity 81.8%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 AARASGPGGGAP 12
Db 91 AARASGPGGTGAP 101
|||||
```

RESULT 5

```
US-11-096-568A-22334
; Sequence 22334, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22334
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(353)
; OTHER INFORMATION: Ceres Seq. ID no. 12408544
US-11-096-568A-22334
```

```
Query Match 69.1%; Score 47; DB 7; Length 353;
Best Local Similarity 69.2%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 AARASGPGGGAPR 13
Db 108 AARASGPGGGAPR 120
|||||
```

RESULT 6

```
US-11-096-568A-22333
; Sequence 22333, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22333
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(358)
; OTHER INFORMATION: Ceres Seq. ID no. 12408543
US-11-096-568A-22333
```

```
Query Match 69.1%; Score 47; DB 7; Length 358;
Best Local Similarity 69.2%; Pred. No. 13;
```

Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AARSGPGGAPR 13
||| ||| |||
Db 113 AARGQPGGQPR 125

RESULT 7

US-11-096-568A-22332
; Sequence 22332, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22332
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(420)
; OTHER INFORMATION: Ceres Seq. ID no. 12408542
US-11-096-568A-22332

Query Match 69.1%; Score 47; DB 7; Length 420;
Best Local Similarity 69.2%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AARSGPGGAPR 13
||| ||| ||| |||
Db 175 AARGQPGGQPR 187

RESULT 8

US-11-096-568A-23806
; Sequence 23806, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23806
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(134)
; OTHER INFORMATION: Ceres Seq. ID no. 12415289
US-11-096-568A-23806

Query Match 67.6%; Score 46; DB 7; Length 134;
Best Local Similarity 72.7%; Pred. No. 7.3;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ARASGPGGAP 12
||| : ||| |||
Db 69 ARGAGPGAGAP 79

RESULT 9

US-11-072-512-3295
; Sequence 3295, Application US/11072512
; Publication No. US20060029945A1

; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3295
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3295

Query Match 66.2%; Score 45; DB 7; Length 678;
Best Local Similarity 80.0%; Pred. No. 41;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RASGPGGAP 12
||| : ||| |||
Db 592 RAAGPGGWP 601

RESULT 10

US-11-109-156-16
; Sequence 16, Application US/11109156
; Publication No. US20050250144A1
; GENERAL INFORMATION:
; APPLICANT: Toshio Ota
; APPLICANT: Takao Isogai
; APPLICANT: Tetsuo Nishikawa
; APPLICANT: Koji Hayashi
; APPLICANT: Kaoru Otsuka
; APPLICANT: Jun-ichi Yamamoto
; APPLICANT: Shizuko Ishii
; APPLICANT: Tomoyasu Sugiyama
; APPLICANT: Ai Wakamatsu
; APPLICANT: Keiichi Nagai
; APPLICANT: Tetsuji Otsuki
; APPLICANT: Shin-ichi Funahashi
; APPLICANT: Chiaki Senoo
; APPLICANT: Jun-ichi Nezu
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN
; FILE REFERENCE: 06501-099002
; CURRENT APPLICATION NUMBER: US/11/109,156
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: US/10/060,065
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05061
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590

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; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-156-16
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Query Match          64.7%; Score 44; DB 7; Length 379;
Best Local Similarity 69.2%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 1 AARASGPGGGAPR 13
Db 3 AAAAQGGGGGPR 15
```

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RESULT 11
US-11-096-568A-26217
; Sequence 26217, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26217
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(558)
; OTHER INFORMATION: Ceres Seq. ID no. 13498878
US-11-096-568A-26217
```

```
Query Match          64.7%; Score 44; DB 7; Length 558;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 2 ARASGPGGGAPR 13
Db 389 ARQEGPAGGPR 400
```

```
RESULT 12
US-10-531-036-35
; Sequence 35, Application US/10531036
; Publication No. US20060015951A1
; GENERAL INFORMATION:
; APPLICANT: Eulenberg, Karsten
; APPLICANT: Weise, Martin
; APPLICANT: Molitor, Andreas
; APPLICANT: Steuernagel, Arnd
; TITLE OF INVENTION: Proteins Involved in the Regulation of Energy Homeostasis
; FILE REFERENCE: 2923-696
; CURRENT APPLICATION NUMBER: US/10/531,036
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: PCT/EP03/11352
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; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: EP 02024747.4
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: EP 02023560.2
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: EP 02022880.5
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-531-036-35
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Query Match          64.7%; Score 44; DB 6; Length 974;
Best Local Similarity 71.4%; Pred. No. 76;
Matches 10; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
```

```
QY 1 AARASG--PGGGAP 12
Db 4 AGRAGGPPPGGGAP 17
```

```
RESULT 13
US-11-096-568A-27265
; Sequence 27265, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27265
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(413)
; OTHER INFORMATION: Ceres Seq. ID no. 15180691
US-11-096-568A-27265
```

```
Query Match          63.2%; Score 43; DB 7; Length 413;
Best Local Similarity 72.7%; Pred. No. 49;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 ARASGPGGGAP 12
Db 95 ARRRGPGGAAP 105
```

```
RESULT 14
US-11-096-568A-641
; Sequence 641, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 641
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
```



```
; LOCATION: (1)..(162)
; OTHER INFORMATION: Ceres Seq. ID no. 12635935
US-11-096-568A-641

Query Match      61.8%; Score 42; DB 7; Length 162;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 AARASGPGGGAP 12
Db      41 AARSGGGGGRRP 52

RESULT 15
US-11-096-568A-23045
; Sequence 23045, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23045
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(249)
; OTHER INFORMATION: Ceres Seq. ID no. 12411110
US-11-096-568A-23045

Query Match      61.8%; Score 42; DB 7; Length 249;
Best Local Similarity 69.2%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 AARASGPGGGAPR 13
Db      18 AARGKGGGGGANR 30

Search completed: March 13, 2006, 20:03:31
Job time : 9.87059 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 18:52:59 ; Search time 90.3529 Seconds

(without alignments)
58.355 Million cell updates/sec

Title: US-09-529-206E-29

Perfect score: 64

Sequence: 1 ARASGGPGGAPR 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	100.0	12	2 AAY06065	Aay06065 Human can
2	64	100.0	13	2 AAY06064	Aay06064 Human can
3	64	100.0	14	2 AAY05986	Aay05986 Human can
4	64	100.0	15	2 AAY05978	Aay05978 Human can
5	64	100.0	20	2 AAY05979	Aay05979 Human can
6	64	100.0	30	5 AAU85105	AAu85105 Human NYN
7	64	100.0	179	8 ADK68648	Adk68648 Epitope 1
8	64	100.0	180	2 AAW62584	Aaw62584 Cancer as
9	64	100.0	180	2 AAW69665	Aaw69665 Human NY-
10	64	100.0	180	2 AAY05965	Aay05965 Human can
11	64	100.0	180	3 AAY52430	Aay52430 Human tum
12	64	100.0	180	3 AAY70862	Aay70862 Human tum
13	64	100.0	180	3 AAB03154	Aab03154 Human oes
14	64	100.0	180	4 AAB69946	Aab69946 Human NY-
15	64	100.0	180	4 AAG67164	Aag67164 Amino aci
16	64	100.0	180	4 AAU01535	AAu01535 Human NY-
17	64	100.0	180	4 AAE07714	AAe07714 Human NY
18	64	100.0	180	5 AAU84818	AAu84818 Human NYN
19	64	100.0	180	5 AAU11543	AAu11543 Human tum
20	64	100.0	180	6 ABR58672	Abr58672 Human can
21	64	100.0	180	6 ABR48210	Abr48210 Human bla
22	64	100.0	180	6 ABU56508	ABu56508 Lung canc
23	64	100.0	180	6 ABU56694	ABu56694 Lung canc
24	64	100.0	180	6 ABP74198	ABp74198 Human NY-

25	64	100.0	180	6 ABU64816	ABu64816 Human NY-
26	64	100.0	180	6 ABR83438	ABr83438 Human NY-
27	64	100.0	180	7 ADC09576	ADc09576 NY-ESO-1
28	64	100.0	180	7 ADD35564	ADd35564 Human NY-
29	64	100.0	180	7 ADD35568	ADd35568 Human NY-
30	64	100.0	180	7 ADD25510	ADd25510 Binding d
31	64	100.0	180	7 ADN39068	ADn39068 Cancer/an
32	64	100.0	180	8 ADJ54139	ADj54139 Human NY-
33	64	100.0	180	8 ADM72815	ADm72815 Human NY-
34	64	100.0	180	8 ADM73418	ADm73418 CAG-3 pro
35	64	100.0	180	8 ADM73417	ADm73417 Human NY-
36	64	100.0	180	8 ADQ18451	ADq18451 Human sof
37	64	100.0	180	8 ADQ10446	ADq10446 Autoimmun
38	64	100.0	180	8 ADS80926	ADs80926 Tumour as
39	64	100.0	180	9 ADW44353	ADw44353 Human aut
40	64	100.0	180	9 ADY85096	ADy85096 Tumour ant
41	64	100.0	180	9 ADZ28913	ADz28913 NY-ESO-1
42	64	100.0	180	9 ADZ42374	ADz42374 Immunogen
43	64	100.0	180	9 AEA35651	AEa35651 Human NY-
44	64	100.0	240	9 ADM99402	ADw99402 NY-ESO-1/
45	64	100.0	240	9 AEB80047	AEb80047 Human NY-

ALIGNMENTS

RESULT 1

AAy06065

ID AAY06065 standard; peptide; 12 AA.

XX AC AAY06065;

XX DT 16-AUG-1999 (first entry)

XX DE Human cancer antigen NY ESO-1/CAG-3 peptide.

XX KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;

XX KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;

XX KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;

XX KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;

XX KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;

XX KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;

XX KW vaccine; cytotoxic T lymphocyte; CTL.

XX OS Homo sapiens.

XX PN WO9918206-A2.

XX PD 15-APR-1999.

XX PF 21-SEP-1998; 98WO-US019609.

XX PR 08-OCT-1997; 97US-0061428P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Wang RF, Rosenberg SA;

XX DR WPI; 1999-277270/23.

XX PT Cancer antigen NY ESO1/CAG-3.

XX PS Example 11; Page 50; 88pp; English.

XX CC This peptide corresponds to amino acid residues 51-62 of human NY ESO-

1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is

capable of eliciting an antigen specific immune response by T cells.

CC Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3

and their variants, are useful as cancer vaccines. A claimed method of

CC preventing or inhibiting cancer involves administering a cancer peptide,

CC with or without an HLA molecule. The cancer peptides form part of, or are

CC derived from, cancers such as primary or metastatic melanoma, thymoma,

CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,

CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 CC as breast, prostate, ovarian, pancreatic and thyroid cancers
 XX
 SQ Sequence 12 AA;

Query Match 100.0%; Score 64; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.049;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
 |||||
 DB 1 ARASGPGGGAPR 12

RESULT 2
 AAY06064
 ID AAY06064 standard; peptide; 13 AA.

XX AAY06064;

DT 16-AUG-1999 (first entry)

Human cancer antigen NY ESO-1/CAG-3 peptide.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine; cytotoxic T lymphocyte; CTL.

OS Homo sapiens.

XX WO9918206-A2.

PN 15-APR-1999.

PF 21-SEP-1998; 98WO-US019609.

PR 08-OCT-1997; 97US-0061428P.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Wang RF, Rosenberg SA;

DR WPI; 1999-277270/23.

XX Cancer antigen NY ESO1/CAG-3.

PS Example 11; Page 50; 88pp; English.

XX This peptide corresponds to amino acid residues 50-62 of human NY ESO-1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is capable of eliciting an antigen specific immune response by T cells.
 CC Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers

SQ Sequence 13 AA;
 Query Match 100.0%; Score 64; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.052;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
 |||||
 DB 2 ARASGPGGGAPR 13

RESULT 3
 AAY05986

ID AAY05986 standard; peptide; 14 AA.

XX AAY05986;

DT 16-AUG-1999 (first entry)

XX Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine.

OS Homo sapiens.

XX WO9918206-A2.

PN 15-APR-1999.

PF 21-SEP-1998; 98WO-US019609.

PR 08-OCT-1997; 97US-0061428P.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Wang RF, Rosenberg SA;

DR WPI; 1999-277270/23.

XX Cancer antigen NY ESO1/CAG-3.

PS Claim 25; Page 50; 88pp; English.

XX The present sequence represents a cancer peptide that corresponds to amino acid residues 49-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-87), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent return to a patient

SQ Sequence 14 AA;

Query Match 100.0%; Score 64; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.056;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
 |||||
 DB 3 ARASGPGGGAPR 14

RESULT 4
 AAY05978

ID AAY05978 standard; peptide; 15 AA.
 AC AAY05978;
 XX
 DT 16-AUG-1999 (first entry)
 DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
 XX
 KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO9918206-A2.
 XX
 PD 15-APR-1999.
 XX
 PP 21-SEP-1998; 98WO-US019609.
 XX
 PR 08-OCT-1997; 97US-0061428P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Wang RF, Rosenberg SA;
 XX
 DR WPI; 1999-277270/23.
 XX
 PT Cancer antigen NY ESO1/CAG-3.
 XX
 PS Claim 15; Page 64; 88pp; English.
 XX
 CC The present sequence represents a cancer peptide that corresponds to
 CC amino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
 CC AAY05965), a new and potent tumour antigen capable of eliciting an
 CC antigen specific immune response by T cells. Cancer peptides derived from
 CC CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
 CC variants (see AAY05967-87), are useful as cancer vaccines that protect
 CC against cancer. The invention provides: vectors and host cells (also
 CC useful as vaccines); a method of diagnosis of cancer or precancer; a
 CC transgenic animal; antisense oligonucleotides that inhibit expression of
 CC the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
 CC cancer peptide, useful in diagnostic and detection assays; and methods
 CC for preventing or inhibiting cancer by administering a cancer peptide,
 CC with or without an HLA molecule. The cancer peptides form part of, or are
 CC derived from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
 CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
 CC treated by inducing cancer-specific T cells in vitro for subsequent
 CC return to a patient
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 64; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.059;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARASGPGGGAPR 12
 |||||
 Db 4 ARASGPGGGAPR 15
 RESULT 5
 AAY05979
 ID AAY05979 standard; peptide; 20 AA.
 XX
 AC AAY05979;
 XX

DT 16-AUG-1999 (first entry)
 XX
 DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
 XX
 KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO9918206-A2.
 XX
 PD 15-APR-1999.
 XX
 PP 21-SEP-1998; 98WO-US019609.
 XX
 PR 08-OCT-1997; 97US-0061428P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Wang RF, Rosenberg SA;
 XX
 DR WPI; 1999-277270/23.
 XX
 PT Cancer antigen NY ESO1/CAG-3.
 XX
 PS Claim 16; Page 64; 88pp; English.
 XX
 CC The present sequence represents a cancer peptide that is based on amino
 CC acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY05965),
 CC a new and potent tumour antigen capable of eliciting an antigen specific
 CC immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-
 CC 3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-
 CC 87), are useful as cancer vaccines that protect against cancer. The
 CC invention provides: vectors and host cells (also useful as vaccines); a
 CC method of diagnosis of cancer or precancer; a transgenic animal;
 CC antisense oligonucleotides that inhibit expression of the cancer peptide
 CC or tumour antigen; antibodies reacting with a CAG-3 cancer peptide,
 CC useful in diagnostic and detection assays; and methods for preventing or
 CC inhibiting cancer by administering a cancer peptide, with or without an
 CC HLA molecule. The cancer peptides form part of, or are derived from,
 CC sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
 CC cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
 CC prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by
 CC inducing cancer-specific T cells in vitro for subsequent return to a
 CC patient
 XX
 SQ Sequence 20 AA;
 Query Match 100.0%; Score 64; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.076;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARASGPGGGAPR 12
 |||||
 Db 9 ARASGPGGGAPR 20
 RESULT 6
 AAU85105
 ID AAU85105 standard; peptide; 30 AA.
 XX
 AC AAU85105;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human NYNSO1a segment 4.

XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW viral infection; human immunodeficiency virus; melanoma;
KW bacterial infection; Salmonella; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
OS Homo sapiens.
XX WO200190197-A1.
XX 29-NOV-2001.
XX 25-MAY-2001; 2001WO-AU000622.
XX 26-MAY-2000; 2000AU-00007761.
XX (AUSU) UNIV AUSTRALIAN NAT.
XX Thomson SA, Ramshaw IA;
XX WPI; 2002-147575/19.
XX N-PSDB; ABK36925.
XX New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
XX Example 3; Fig 27; 364pp; English.
XX The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC cesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcus, Haemophilus,
CC Salmonella, Streptococcus, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a Savine of the
XX invention
XX Sequence 30 AA;
SQ
Query Match 100.0%; Score 64; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARASGPGGGAPR 12
Db 8 ARASGPGGGAPR 19
RESULT 7
ADK68648
ID ADK68648 standard; protein; 179 AA.
XX ADK68648;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX

DE Epitope liberation-related NY-ESO-1 protein SeqID11.
XX
KW epitope liberation; substrate; proteasome; cytostatic; antibacterial;
KW prozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope;
KW cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;
KW virus; bacterium; protozoan; fungus; housekeeping proteasome system;
KW human.
XX Homo sapiens.
OS
XX US2003228634-A1.
XX 11-DEC-2003.
XX 07-NOV-2002; 2002US-00292413.
XX 07-NOV-2001; 2001US-0336968P.
XX (SIMA/) SIMARD J J L.
PA (DIAM/) DIAMOND D C.
PA (QIUZ/) QIU Z.
PA (LEIX/) LEI X.
XX Simard J J L, Diamond DC, Qiu Z, Lei X;
XX WPI; 2004-167209/16.
DR N-PSDB; ADK68674.
XX
XX Identifying polypeptide suitable for epitope e.g., housekeeping epitope,
PT liberation by contacting substrate polypeptide comprising epitope of
PT interest, with proteasome, and assaying for liberation of epitope.
XX
XX Example 2; SEQ ID NO 11; 67pp; English.
XX This invention relates to a novel method of identifying a polypeptide
CC suitable for epitope liberation, including the steps of identifying an
CC epitope of interest; providing substrate polypeptide sequence including
CC the epitope, wherein the substrate permits processing by a proteasome;
CC contacting the substrate with a composition including the proteasome;
CC under conditions that support processing of the substrate by proteasome;
CC and assaying for liberation of epitope. The invention may be useful for
CC the development of compounds with a cytostatic, antibacterial,
CC prozoacide or fungicide activity acting as T-cell activators. In
CC addition, the invention may allow development of a vaccine. The invention
CC is useful for identifying a polypeptide suitable for epitope liberation,
CC where the epitope is a housekeeping epitope. The compositions comprising
CC the identified housekeeping epitopes are useful in vitro in vaccine
CC development or in the generation or expansion of cytotoxic T lymphocyte
CC (CTL) to be used in adoptive immunotherapy. The invention is also useful
CC for activating T-cells against neoplastic cells, and cells infected with
CC virus, bacterium, protozoan or fungus. CTL epitopes are identified based
CC on the knowledge that such epitopes are, in fact, produced by the
CC housekeeping proteasome system. Once identified, these epitopes, embodied
CC as peptides, can be used to successfully immunise or induce therapeutic
CC CTL responses against housekeeping proteasome expressing target cells in
CC the host. The present sequence is that of a protein which is related to
CC the method of the invention.
XX
XX Sequence 179 AA;
SQ
Query Match 100.0%; Score 64; DB 8; Length 179;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARASGPGGGAPR 12
Db 50 ARASGPGGGAPR 61
RESULT 8
AAW62584
ID AAW62584 standard; protein; 180 AA.
XX

AAW62584;
 17-SEP-1998 (first entry)
 Cancer associated antigen NY-ESO-1.
 Cancer associated antigen; NY-ESO-1; regression; progression; onset;
 cancer; treatment; diagnosis.
 Homo sapiens.
 Key Location/Qualifiers
 Misc-difference 7 /note= "potential myristoylation site"
 Misc-difference 9 /note= "potential myristoylation site"
 Misc-difference 11 /note= "potential phosphorylation site"
 Misc-difference 98 /note= "potential phosphorylation site"
 Misc-difference 134 /note= "potential phosphorylation site"
 Misc-difference 138 /note= "potential phosphorylation site"
 Misc-difference 138 /note= "potential phosphorylation site"
 WO9814464-A1.
 09-APR-1998.
 15-SEP-1997; 97WO-US016335.
 03-OCT-1996; 96US-00725182.
 (LUDW-) LUDWIG INST CANCER RES.
 Chen Y, Scanlan M, Gure A, Old LJ, Jager E, Knuth A;
 Drijfhout JW;
 WPI; 1998-286417/25.
 N-PSDB; AAV38566.
 New isolated cancer associated antigen - is used to develop products for
 the diagnosis and treatment of cancers and for monitoring cancer therapy.
 Claim 8; Fig 3; 49pp; English.
 The present sequence represents a cancer associated antigen. The clone
 from which the DNA sequence is obtained is designated NY-ESO-1. The
 specification described a method for determining regression, progression
 of onset of a cancerous condition, comprising monitoring a sample from a
 patient with the cancerous condition for a parameter selected from NY-ESO
 -1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells
 specific for the peptide and an MHC molecule with which it non-covalently
 complexes. Methods for the treatment of a cancerous condition are also
 described. The NY-ESO-1 protein and peptides derived from it can be used
 for diagnosis and treatment of cancers and to monitor the efficacy of a
 therapeutic regime

Query Match 100.0%; Score 64; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.51;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
 |||||
 Db 51 ARASGPGGGAPR 62

RESULT 9
 AAW62584
 ID AAW62584 standard; protein; 180 AA.
 XX

AAW69665;
 27-OCT-1998 (first entry)
 Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
 Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
 Homo sapiens.
 WO9832855-A1.
 30-JUL-1998.
 27-JAN-1998; 98WO-US001445.
 27-JAN-1997; 97US-00791495.
 (LUDW-) LUDWIG INST CANCER RES.
 Lethe B, Lucas S, De Smet C, Godelaine D, Boon-Palleur T;
 WPI; 1998-427951/36.
 N-PSDB; AAV50348.
 New isolated LAGE-1 tumour associated nucleic acids - used to develop
 products for the diagnosis and treatment of LAGE-1 associated disorders,
 particularly tumours.
 Example 2; Page 57-58; 73pp; English.
 The present sequence represents human NY-ESO-1, formerly known as LL-1.2
 clone, which is used in an example from the present invention which
 describes LAGE-1 tumour associated protein (TAP). The present invention
 also describes: (1) a method for treating a subject with a disorder
 characterised by expression of a LAGE-1 nucleic acid molecule or an
 expression product, comprising administering to the subject autologous
 cytolytic T cells to ameliorate the disorder, where the cytolytic T cells
 are specific for complexes of an HLA molecule and a LAGE-1 TAP or an
 immunogenic fragment; (2) a method for treating a subject with a disorder
 characterised by expression of a LAGE-1 nucleic acid molecule or an
 expression product, comprising administering a LAGE-1 TAP or an
 immunogenic fragment to ameliorate the disorder; and (3) a method for
 selectively enriching a population of T cells with cytolytic T cells
 specific for a LAGE-1 TAP comprising contacting an isolated population of
 T cells with an agent presenting a complex of a LAGE TAP or an
 immunogenic fragment and a HLA presenting molecule to selectively enrich
 the isolated population of T cells with the cytolytic T cells. The
 methods and products from the present invention can be used for the
 diagnosis and treatment of LAGE-1 associated disorders, particularly
 tumours

Query Match 100.0%; Score 64; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.51;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
 |||||
 Db 51 ARASGPGGGAPR 62

RESULT 10
 AAY05965
 ID AAY05965 standard; protein; 180 AA.
 XX
 AC AAY05965;
 XX
 DT 16-AUG-1999 (first entry)
 XX Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.
 XX


```

FT Peptide 159..167
FT /note= "Peptide presented by MHC Class I HLA-A3"
FT Peptide 162..170
FT /note= "Peptide presented by MHC Class I HLA-B52"
XX
XX WO9953938-A1.
XX
XX 28-OCT-1999.
XX
XX 24-MAR-1999; 99WO-US006875.
XX
XX 17-APR-1998; 98US-00062422.
XX 02-OCT-1998; 98US-00165546.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
XX Gure A, Ritter G;
XX
XX WPI; 2000-038483/03.
XX N-PSDB; AAZ38380.
XX
XX Novel peptides which bind to MHC class I and MHC class II molecules,
XX useful for therapeutic and diagnostic purposes.
XX
XX Claim 30; Fig 3; 49pp; English.
XX
XX This sequence represents a human tumour antigen, NY-ESO-1, the cDNA
XX encoding which was isolated from an oesophagus squamous cell cancer cDNA
XX library. Tissue localisation studies revealed it to be expressed at high
XX levels in normal ovary and testis but not in normal colon, kidney, liver,
XX brain, oesophagus and skin. It was expressed in certain tumours and
XX tumour cell lines with some degree of frequency - these included melanoma
XX specimens and cell lines, and breast and bladder cancer specimens, with
XX expression in other tumour types being sporadic. Peptides derived from NY
XX -ESO-1 are bound by both MHC (major histocompatibility complex) Class I
XX and Class II molecules for presentation to T-cells. Peptides AAY52431-
XX Y52434 bind to Class I HLA-A2 molecules, thereby stimulating
XX proliferation of cytotoxic T-cells, while peptides AAY52435-Y52440 bind
XX to Class II HLA-DR3 molecules, stimulating helper T-cell proliferation.
XX The peptides derived from NY-ESO-1 may be used in methods and
XX compositions used for the treatment, diagnosis and prevention of cancers
XX (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma,
XX ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to
XX stimulate the proliferation of T cells
XX
XX Revised record issued on 21-OCT-2004 : Correction to feature table key
XX
XX Sequence 180 AA;
XX
XX Query Match 100.0%; Score 64; DB 3; Length 180;
XX Best Local Similarity 100.0%; Pred. No. 0.51;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ARASGPGGGAPR 12
XX |||||
XX Db 51 ARASGPGGGAPR 62
XX
XX RESULT 12
XX AAY70862
XX ID AAY70862 standard; protein; 180 AA.
XX
XX AC AAY70862;
XX
XX 31-JUL-2000 (first entry)
XX
XX Human tumour antigen, NY-ESO-1 protein.
XX
XX NY-ESO-1; CAMEL; CTL-recognised Antigen on MELANOMA; human; cancer; CTL;
XX cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer;
XX melanoma; immunotherapy; immune response.
XX

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```

OS Homo sapiens.
XX
XX WO200023584-A1.
XX
XX 27-APR-2000.
XX
XX 15-OCT-1999; 99WO-EP007832.
XX
XX 16-OCT-1998; 98EP-00119583.
XX
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX (UYHO-) UNIV HOSPITAL LEIDEN.
XX
XX Schrier PI, Aarnoudse CA, Heider K, Klade C;
XX
XX WPI; 2000-339685/29.
XX N-PSDB; AAD00152.
XX
XX Tumor-associated antigen useful for cancer immunotherapy is encoded by
XX the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
XX
XX Example 3; Page 62-63; 73pp; English.
XX
XX The present sequence is the human NY-ESO-1 protein, a tumour antigen,
XX identified by screening an esophagus carcinoma cDNA library. This protein
XX is derived from open reading frame (ORF)-1 that contain epitopes of
XX tumour specific T-cells. NY-ESO-1 is expressed in different tumour types,
XX but not in healthy tissues except in testis. It also shows homology with
XX the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELANOMA)
XX protein, a tumour-associated antigen. The tumour-associated antigen
XX displayed on melanoma cells is recognised by cytotoxic T lymphocytes.
XX This sequence has anticancer activity. CAMEL tumour antigen and
XX immunogenic peptides derived from it are useful for cancer immunotherapy.
XX They have the potential to induce an immune response, by eliciting a CTL
XX response. The DNA molecule is used for the construction of recombinant or
XX fusion proteins
XX
XX Sequence 180 AA;
XX
XX Query Match 100.0%; Score 64; DB 3; Length 180;
XX Best Local Similarity 100.0%; Pred. No. 0.51;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ARASGPGGGAPR 12
XX |||||
XX Db 51 ARASGPGGGAPR 62
XX
XX RESULT 13
XX AAB03154
XX ID AAB03154 standard; protein; 180 AA.
XX
XX AC AAB03154;
XX
XX 23-OCT-2000 (first entry)
XX
XX Human oesophageal cancer-associated antigen NY-ESO-1.
XX
XX Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen;
XX oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain;
XX antibody; diagnostic marker; drug delivery target.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Modified-site 7
XX FT /note= "Potential N-myristoylation site"
XX FT Modified-site 9
XX FT /note= "Potential N-myristoylation site"
XX FT Modified-site 11
XX FT /note= "Potential O-phosphorylation site"
XX FT Modified-site 98
XX FT /note= "Potential O-phosphorylation site"
XX

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FT Modified-site 134 /note= "Potential O-phosphorylation site"
FT Modified-site 138 /note= "Potential O-phosphorylation site"
FT FT 152..172
FT Domain /note= "Potential transmembrane domain"
FT XX
FN US6069233-A.
FN XX
FD 30-MAY-2000.
FD XX
PP 26-JAN-1998; 98US-00013150.
PP XX
PR 03-OCT-1996; 96US-00725381.
PR XX
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
PA (CORR ) CORNELL RES FOUND INC.
PA (LUDW-) LUDWIG INST CANCER RES.
PA XX
PI Scanlan M, Gure AO, Chen Y, Tureci O, Sahin U, Pfreundschuh M;
PI Old LJ;
PI XX
DR WPI; 2000-410880/35.
DR N-PSDB; AAF61483.
DR XX
PT New isolated esophageal cancer-associated antigen useful as markers for
PT producing antibodies and as targets for identifying abnormal conditions,
PT e.g. infections and cancer.
PT XX
PS Example 5; Fig 3; 9pp; English.
PS XX
CC This sequence represents a human oesophageal cancer-associated antigen,
CC NY-ESO-1. The cDNA encoding this sequence was isolated from a cDNA
CC library prepared from a specimen of well-to-moderately differentiated
CC squamous cell cancer of the oesophagus. Expression analysis demonstrated
CC that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma
CC cell lines and in normal ovary and testis tissue, but not in normal
CC colon, kidney, liver or brain tissue. Analysis of the amino acid sequence
CC of the protein indicates that the protein has a transmembrane domain,
CC several N-myristoylation sites and O-phosphorylation sites and that it
CC contains antigenic sequences in the N-terminal half of the protein. The
CC antigen is useful as an immunogen when combined with an adjuvant, in both
CC precursor and post- translationally modified forms, and may be used to
CC generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic
CC marker for oesophageal cancer, and can be utilised as a marker for the
CC targeted delivery of therapeutic agents to oesophageal cancer cells. It
CC can also be used to generate diagnostic or therapeutic agents
CC XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 64; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
Db |||||
51 ARASGPGGGAPR 62

RESULT 14
AAB69946
ID AAB69946 standard; protein; 180 AA.
XX
AC AAB69946;
XX
DT 27-APR-2001 (first entry)
XX
DE Human NY-ESO-1 protein.
XX
KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW non-small cell lung carcinoma; tumour status determination.
XX

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OS Homo sapiens.
XX WO200107917-A1.
XX PD 01-FEB-2001.
XX PF 14-JUL-2000; 2000WO-US019220.
XX PR 23-JUL-1999; 99US-00359503.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX PA (CORR ) CORNELL RES FOUND INC.
XX PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
XX WPI; 2001-182822/18.
XX DR N-PSDB; AAF58634.
XX PT Method useful for determining the status (e.g. progression, regression or
PT stability of the disease) of a cancerous condition, involves determining
PT the levels of NY-ESO-1 specific antibodies in a sample taken from a
PT patient.
XX PS Example 5; Fig 3; 50pp; English.
XX CC The present sequence is human NY-ESO-1 protein. It is provided in a
CC specification relating to a method for determining the status of a
CC cancerous condition in a patient with a tumour that expresses NY-ESO-1.
CC The method comprises assaying a sample taken from the patient for
CC antibodies that specifically bind to the NY-ESO-1 and comparing the value
CC obtained to a prior value obtained from assay of a prior sample taken
CC from the patient. Any difference between the values is indicative of a
CC change in status of the cancerous condition. The method is useful for
CC determining whether a cancerous condition is progressing, regressing or
CC remaining stable, in particular in patients receiving treatment for a
CC melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
CC carcinoma
XX SQ Sequence 180 AA;

Query Match 100.0%; Score 64; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
Db |||||
51 ARASGPGGGAPR 62

RESULT 15
AAG67164
ID AAG67164 standard; protein; 180 AA.
XX
AC AAG67164;
XX DT 13-NOV-2001 (first entry)
XX DE Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
XX KW Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
XX KW HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour;
XX KW cancer; testis tumour.
XX OS Homo sapiens.
XX PN WO200162917-A1.
XX PD 30-AUG-2001.
XX PF 22-JAN-2001; 2001WO-US002126.
XX PR 22-FEB-2000; 2000US-00510635.

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XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Lethe B, Boon-Falleur T;
XX
XX WPI; 2001-550091/61.
XX DR N-PSDE; AAH75118.
XX
XX Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful
XX for diagnosing testicular tumors.
XX
XX Example 5; Fig 3; 50pp; English.
XX
XX The present sequence represents cancer testis tumour antigen NY-ESO-1
XX (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at
XX least one human leukocyte antigen (HLA) binding peptide, which binds to
XX Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is
XX expressed in tumour mRNA and in testis, but not normal colon, kidney,
XX liver or brain tissue. The presence or level of expression of NY-ESO-1
XX may be assayed for the diagnosis of cancer, especially testis tumours
XX
XX SQ Sequence 180 AA;
XX
XX Query Match 100.0%; Score 64; DB 4; Length 180;
XX Best Local Similarity 100.0%; Pred. NO. 0.51;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ARASGPGGGAPR 12
XX |||||||||
XX Db 51 ARASGPGGGAPR 62

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Search completed: March 13, 2006, 19:03:59
 Job time : 90.3529 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:04:24 ; Search time 14.2588 Seconds
(without alignments)
80.975 Million cell updates/sec

Title: US-09-529-206E-29
Perfect score: 64
Sequence: 1 ARASGPGGAPR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	44	68.8	3190	T13828	CREB-binding prote
2	42	65.6	185	T36874	hypothetical prote
3	42	65.6	201	G72663	hypothetical prote
4	42	65.6	222	T36115	probable oxidoredu
5	42	65.6	327	T29031	hypothetical prote
6	42	65.6	351	S50754	hypothetical prote
7	42	65.6	378	C87425	aldose 1-epimerase
8	42	65.6	436	T36104	conserved hypothet
9	42	65.6	474	G75580	conserved hypothet
10	41	64.1	173	AB3648	flagellar basal-bo
11	41	64.1	286	S04673	H+-transporting tw
12	41	64.1	357	F82878	XAA-PRO aminopepti
13	41	64.1	371	T39312	hypothetical prote
14	41	64.1	505	S68518	tub protein, brain
15	41	64.1	521	A29345	steroid hormone re
16	41	64.1	1207	T00378	KIAA0641 protein -
17	41	64.1	1690	T35694	ATP dependent DNA
18	40	62.5	82	T04476	acclimation protei
19	40	62.5	290	T36712	hypothetical prote
20	40	62.5	335	S08341	myristylated alani
21	40	62.5	379	A48082	MAP kinase 3 (EC 2
22	40	62.5	383	A86182	hypothetical prote
23	40	62.5	679	S02165	regulatory protein
24	40	62.5	910	A34721	androgen receptor
25	40	62.5	911	B34721	androgen receptor
26	40	62.5	919	A39248	androgen receptor
27	40	62.5	954	A87431	regulatory protein
28	39.5	61.7	730	A36226	collagen alpha 1 c
29	39	60.9	103	C72683	hypothetical prote

30	39	60.9	114	2	B45036	Pur beta - human (
31	39	60.9	163	2	E87464	competence/damage-
32	39	60.9	166	2	I69006	histocompatibility
33	39	60.9	187	2	T35619	hypothetical prote
34	39	60.9	197	2	S25825	polygalacturonase
35	39	60.9	213	2	S42585	DNA-invertase - Rh
36	39	60.9	260	2	F95899	probable transcrip
37	39	60.9	269	2	A47008	transcription acti
38	39	60.9	306	2	S25824	polygalacturonase
39	39	60.9	307	2	B72677	hypothetical prote
40	39	60.9	349	2	S55626	hypothetical prote
41	39	60.9	377	2	S28184	Ca2+/calmodulin-de
42	39	60.9	380	2	JC1451	Ca2+/calmodulin-de
43	39	60.9	387	2	T52451	endopeptidase Clp
44	39	60.9	410	2	S30067	polygalacturonase
45	39	60.9	410	2	S30066	polygalacturonase

ALIGNMENTS

RESULT 1

T13828
CREB-binding protein homolog - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13828
R:Akimaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; G.
Nature 386, 735-738, 1997
A:Title: Drosophila CBP is a co-activator of cubitus interruptus in hedgehog signalling
A:Reference number: Z17785; MUID:97263578; PMID:9109493
A:Accession: T13828
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-3190 <AKI>
A:Cross-references: UNIPROT:O01368; UNIPARC:UPI000003EB83; EMBL:U88570; NID:gl916929; P
C:Genetics:
A:Cross-references: FlyBase:FBgn0015624
A:Map position: X
F:1723-1780/Domain: bromodomain homology <BRO>

Query Match 68.8%; Score 44; DB 2; Length 3190;
Best Local Similarity 77.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 SCFPGGAPR 12
:|||||
DB 320 NGPFGGGPR 328

RESULT 2

T36874
hypothetical protein SC151.11c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T36874
R:Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21617
A:Accession: T36874
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-185 <MUR>
A:Cross-references: UNIPROT:Q9S229; UNIPARC:UPI00000DB31A; EMBL:AL109848; PIDN:CA852835
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC151.11c

Query Match 65.6%; Score 42; DB 2; Length 185;
Best Local Similarity 80.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARASGPGGGA 10

```
Db      86 ARSGPFGGA 95
|||||
f

RESULT 3
G72663
hypothetical protein APE0734 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: G72663
R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A>Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: G72663
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-201 <KAW>
A:Cross-references: UNIPROT:Q9YE35; UNIPARC:UPI000005DC7C; DDBJ:AP000060; NID:G5104188;
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0734
C:Superfamily: Aeropyrum pernix hypothetical protein APE0734

Query Match      65.6%; Score 42; DB 2; Length 201;
Best Local Similarity 75.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 ARASGPGGGAPR 12
|||||
Db      37 ARASGVGRRPR 48

RESULT 4
T36115
probable oxidoreductase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
C:Accession: T36115
R:Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1999
A:Reference number: Z21597
A:Accession: T36115
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-222 <MUR>
A:Cross-references: UNIPROT:Q9X887; UNIPARC:UPI00000DB008; EMBL:AL049707; PIDN:CAB41281.
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCE15.12c
C:Superfamily: NAD(P)H-dependent FMN reductase (sulfate starvation-induced protein 4); S

Query Match      65.6%; Score 42; DB 2; Length 222;
Best Local Similarity 72.7%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 ARASGPGGGAP 11
|||||
Db      183 ARASGPSAGRP 193

RESULT 5
T29031
hypothetical protein F53G12.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29031
R:Wu, X.; Graves, T.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid F53G12.
A:Reference number: Z20555
A:Accession: T29031

A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-327 <WUX>
A:Cross-references: UNIPROT:O01799; UNIPARC:UPI0000078FF; EMBL:AF003139; PIDN:AAB54156.
A:Experimental source: strain Bristol N2; clone F53G12
C:Genetics:
A:Gene: CESP:F53G12.7
A:Map position: 1
A:Introns: 59/3; 138/1; 223/2

Query Match      65.6%; Score 42; DB 2; Length 327;
Best Local Similarity 72.7%; Pred. No. 81;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 ARASGPGGGAP 11
|||||
Db      113 AEAAGGGGGAP 123

RESULT 6
S50754
hypothetical protein WP6 - Chlamydomonas eugametos
C:Species: Chlamydomonas eugametos
C>Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S50754
R:Moessner, J.P.; Molendijk, A.J.; van Egmond, P.; Klis, F.M.; Goodenough, U.W.; Haring,
Plant Mol. Biol. 26, 947-960, 1994
A>Title: Domain conservation in several volvocalean cell wall proteins.
A:Reference number: S50754; MUID:95093034; PMID:8000007
A:Accession: S50754
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-351 <WOE>
A:Cross-references: UNIPROT:Q39492; UNIPARC:UPI00000A170A; EMBL:L29028; NID:G530877; PID

Query Match      65.6%; Score 42; DB 2; Length 351;
Best Local Similarity 80.0%; Pred. No. 86;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 RASGPGGGAP 11
|||||
Db      299 RASPPGGGPP 308

RESULT 7
C87425
aldose 1-epimerase [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: C87425
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A>Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: C87425
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-378 <STO>
A:Cross-references: UNIPROT:Q9A8D6; UNIPARC:UPI00000C73A0; GB:AE005673; NID:G13422779; P

C:Genetics:
A:Gene: CCI418
C:Superfamily: aldose 1-epimerase

Query Match      65.6%; Score 42; DB 2; Length 378;
Best Local Similarity 77.8%; Pred. No. 91;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 SGPGGGAPR 12
|||||
Db      282 NGPSGGAPR 290
```

```
RESULT 8
T36104
conserved hypothetical protein SCB15.01 - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36104
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1999
A;Reference number: Z21597
A;Accession: T36104
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-436 <MUR>
A;Cross-references: UNIPROT:O8CJX1; UNIPARC:UPI000017AD99; EMBL:AL049707; PIDN:CAB41270.
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCE15.01

Query Match 65.6%; Score 42; DB 2; Length 436;
Best Local Similarity 72.7%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

QY 1 ARASGPGGGAP 11
Db 151 ADASGPGGNTF 161

RESULT 9
G75580
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: G75580
R;White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75580
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-474 <WHI>
A;Cross-references: UNIPROT:Q9RYN8; UNIPARC:UPI00000C166F; GB:AE001863; GB:AE001825; NID
A;Experimental source: strain R1
C;Genetics:
A;Gene: DRA0272
A;Map position: 2
C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF0821

Query Match 65.6%; Score 42; DB 2; Length 474;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARASGPGGGA 10
Db 319 ATAGGPGGGA 328

RESULT 10
AB3648
flagellar basal-body rod protein flgF [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AB3648
R;DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
Mazur, M.; Goltzman, E.; Salkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AB3648
A;Status: preliminary
```

```
A;Molecule type: DNA
A;Residues: 1-173 <KUR>
A;Cross-references: UNIPROT:Q8YAZA; UNIPARC:UPI0000058740; GB:AE008918; PIDN:AAL54349.1
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI11107
A;Map position: II

Query Match 64.1%; Score 41; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PGGGAPR 12
Db 132 PGGGAPR 138

RESULT 11
S04673
H+-transporting two-sector ATPase (EC 3.6.3.14) gamma chain - Rhodospseudomonas blastic
C;Species: Rhodospseudomonas blastica
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 31-Dec-2004
C;Accession: S04673
R;Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.
J. Mol. Biol. 179, 185-214, 1984
A;Title: Rhodospseudomonas blastica atp operon. Nucleotide sequence and transcription.
A;Reference number: S04666; MUID:85058188; PMID:6209404
A;Accession: S04673
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-286 <TYB>
A;Cross-references: UNIPROT:P05436; UNIPARC:UPI0000126582
C;Superfamily: H(+)-transporting ATP synthase gamma chain
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

Query Match 64.1%; Score 41; DB 2; Length 286;
Best Local Similarity 80.0%; Pred. No. 99;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ASGPGGGAPR 12
Db 57 ASGPGGAGAPR 66

RESULT 12
F82878
XAA-PRO aminopeptidase UUS32 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: F82878
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a m
A;Reference number: A82870
A;Accession: F82878
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <GLA>
A;Cross-references: UNIPARC:UPI00000C1CAC; GB:AE002152; GB:AF222894; NID:g68999532; PIDN
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: pepP; UUS32
A;Genetic code: SGC3
C;Superfamily: X-Pro aminopeptidase

Query Match 64.1%; Score 41; DB 2; Length 357;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 ASGPGGGAP 11
Db 193 ASGPGGGSP 201
```

RESULT 13

T39312
hypothetical protein SPBC119.14 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39312
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, March 1998
A:Reference number: Z21843
A:Accession: T39312
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-371 <WOO>
A:Cross-references: UNIPROT:O42905; UNIPARC:UPI00001352D5; EMBL:AL022117; PIDN:CAA17929.
A:Experimental source: strain 972h; cosmid c119
C:Genetics:
A:Gene: SPDB:SPBC119.14
A:Map position: 2
A:Introns: 77/3; 105/3; 165/3; 250/1; 276/2

Query Match 64.1%; Score 41; DB 2; Length 371;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARASGPGGGA 10
DB 35 SRRSGPGGS 44
: || || || || |

RESULT 14

368518
tub protein, brain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Nov-1996 #sequence_revision 27-Feb-1997 #text_change 31-Dec-2004
C:Accession: S68518; S68519
R:Noben-Trauth, K.; Nagert, J.K.; North, M.A.; Nishina, P.M.
Nature 380, 534-538, 1996
A:Title: A candidate gene for the mouse mutation tubby.
A:Reference number: S68518; MUID:96195061; PMID:8606774
A:Accession: S68518
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-505 <NOB>
A:Cross-references: UNIPROT:P50586; UNIPARC:UPI000002367A; EMBL:U52433; NID:g1279765; PI
A:Accession: S68519
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 47-505 <NO2>
A:Cross-references: UNIPARC:UPI00001488EE; EMBL:U52824; NID:g1280436; PIDN:AAC52512.1; F
C:Superfamily: tubby

Query Match 64.1%; Score 41; DB 2; Length 505;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
DB 113 AAASGGGGAPR 124
| ||| |||||

RESULT 15

A29345
steroid hormone receptor ERR1 precursor - human
N:Alternate names: estrogen-related receptor
C:Species: Homo sapiens (man)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 31-Dec-2004
C:Accession: A29345; A49074
R:Giguere, V.; Yang, N.; Segui, P.; Evans, R.M.
Nature 331, 91-94, 1988
A:Title: Identification of a new class of steroid hormone receptors.
A:Reference number: A29345; MUID:88122546; PMID:3267207
A:Accession: A29345

A:Molecule type: mRNA

A:Residues: 1-521 <GIG>
A:Cross-references: UNIPROT:P11474; UNIPARC:UPI0000142399; EMBL:X51416; NID:g36608; PIDN:
R:Willey, S.R.; Kraus, R.J.; Zuo, F.; Murray, E.E.; Loritz, K.; Mertz, J.E.
Genes Dev. 7, 2206-2219, 1993
A:Title: SV40 early-to-late switch involves titration of cellular transcriptional repres
A:Reference number: A49074; MUID:94040741; PMID:8224847
A:Accession: A49074
A:Status: preliminary
A:Molecule type: protein
A:Residues: 166-169, 'X', 171-173 <WIL>
A:Cross-references: UNIPARC:UPI000017A1DF
C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; zi
F:174-434/Domain: erba transforming protein homology <ERBA>
F:176-196/Region: zinc finger
F:212-236/Region: zinc finger

Query Match 64.1%; Score 41; DB 2; Length 521;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
DB 462 AGRAGPGGAER 473
| : || || || |

Search completed: March 13, 2006, 19:16:11
Job time : 14.2588 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 18:53:23 ; Search time 87.1059 Seconds
 (without alignments)
 97.196 Million cell updates/sec

Title: US-09-529-206E-29
 Perfect score: 64
 Sequence: 1 ARASGPGGAPR 12

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 70528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	142	Q9NY13_HUMAN	Q9ny13 homo sapien
2	64	100.0	180	CTG1B_HUMAN	P78358 homo sapien
3	64	100.0	180	Q7LBY4_HUMAN	O7lby4 homo sapien
4	56	87.5	210	CTAG2_HUMAN	O75838 homo sapien
5	54	84.4	362	Q63QT8_BURPS	Q63qt8 burkholderi
6	54	84.4	362	Q62H22_BURMA	Q62h22 burkholderi
7	50	78.1	194	Q96BU2_HUMAN	Q96bu2 homo sapien
8	50	78.1	896	Q96D18_HUMAN	Q96d18 homo sapien
9	50	78.1	1253	Q6DHV6_HUMAN	Q6dhv6 homo sapien
10	50	78.1	1430	Q9H7P9_HUMAN	Q9h7p9 homo sapien
11	48	75.0	262	Q528E2_ORYSA	Q528e2 oryza sativ
12	48	75.0	321	Q96S27_HUMAN	Q96s27 homo sapien
13	48	75.0	449	Q7FLE3_ORYSA	Q7fle3 oryza sativ
14	47	73.4	367	Q6AV33_ORYSA	Q6av33 oryza sativ
15	47	73.4	895	Q4NUK4_9DELTA	Q4nuk4 anaeromyxob
16	46	71.9	175	PACA_CHICK	P41534 g glucagon-
17	46	71.9	327	Q63HT9_BURPS	Q63ht9 burkholderi
18	46	71.9	330	Q629N3_BURMA	Q629n3 burkholderi
19	46	71.9	383	Q4TEG9_TETNG	Q4teg9 tetraodon n
20	46	71.9	695	Q4T320_TETNG	Q4t320 tetraodon n
21	46	71.9	708	Q5KJMS_CRYNE	Q5kjms cryptococcu
22	46	71.9	708	Q55WMI_CRYNE	Q55wmi cryptococcu
23	46	71.9	788	Q4QOP8_HUMAN	Q4qop8 homo sapien
24	46	71.9	1000	Q4FKF7_9TRYP	Q4fkf7 trypanosoma
25	45	70.3	309	Q63N33_BURPS	Q63n33 burkholderi
26	45	70.3	322	Q67PJ0_SYNT	Q67pj0 symbiobacte
27	45	70.3	337	Q7LOR6_HUMAN	Q7lor6 homo sapien
28	45	70.3	432	Q7LOR7_HUMAN	Q7lor7 homo sapien
29	45	70.3	444	Q9UPQ2_HUMAN	Q9upq2 homo sapien
30	45	70.3	472	Q51LM2_MAGGR	Q51lm2 magnaporthe
31	45	70.3	504	Q4NVJ7_9DELTA	Q4nvj7 anaeromyxob

32	45	70.3	559	2	Q8L680_ORYSA	Q8l680 oryza sativ
33	45	70.3	678	2	Q8NAC4_HUMAN	Q8nac4 homo sapien
34	45	70.3	730	2	Q4NZ61_9DELTA	Q4nz61 anaeromyxob
35	45	70.3	867	2	Q94LD1_ORYSA	Q94ld1 oryza sativ
36	45	70.3	905	2	Q4NTZ7_9DELTA	Q4ntz7 anaeromyxob
37	45	70.3	1379	2	Q7QEK5_ANOGA	Q7qek5 anopheles g
38	45	70.3	1383	2	Q4SW43_TETNG	Q4sw43 tetraodon n
39	45	70.3	2013	2	Q4NWX4_9DELTA	Q4nwx4 anaeromyxob
40	44	68.8	111	2	Q5NTAS_CANFA	Q5ntas canis famli
41	44	68.8	159	2	Q63KC9_BURPS	Q63kc9 burkholderi
42	44	68.8	159	2	Q62DA7_BURMA	Q62da7 burkholderi
43	44	68.8	159	2	Q4RBL9_TETNG	Q4rbl9 tetraodon n
44	44	68.8	162	2	Q6YUN8_ORYSA	Q6yun8 oryza sativ
45	44	68.8	163	2	Q6AD35_LEIXX	Q6ad35 leifsonia x

ALIGNMENTS

RESULT 1
 Q9NY13_HUMAN PRELIMINARY; PRT; 142 AA.
 AC Q9NY13;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Hypothetical protein LAGE-2 (Fragment).
 GN Name=LAGE-2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Lethe B.G.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ275978; CAB76945.1; -; mRNA.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;

Query Match 100.0%; Score 64; DB 2; Length 142;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARASGPGGAPR 12
 |||||
 DB 25 ARASGPGGAPR 36

RESULT 2
 CTG1B_HUMAN STANDARD; PRT; 180 AA.
 ID CTG1B_HUMAN
 AC P78358;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-ESO-1).
 GN Name=CTAG1B; Synonyms=CTAG, CTAG1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Chen Y.-T., Scanlan M.J., Sahin U., Tuerci O., Gure A.O., Tsang S.,
 Williamon B., Stockert E., Pfundsduh M., Old L.J.;
 RT "A testicular antigen aberrantly expressed in human cancers detected
 by autologous antibody screening.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Melanoma;
 RX MEDLINE=98289662; PubMed=9626360;
 RA Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
 RA de Plaen E., Boon T.;
 RT "LAGE-1, a new gene with tumor specificity.";
 RL Int. J. Cancer 76:903-908(1998).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98430682; PubMed=9759882;
 RA Wang R.-P., Johnston S.L., Zeng G., Topalian S.L.,
 RA Schwartzentruber D.J., Rosenberg S.A.;
 RT "A breast and melanoma-shared tumor antigen: T cell responses to
 RT antigenic peptides translated from different open reading frames.";
 RL J. Immunol. 161:3596-3606(1998).
 CC -1- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide
 CC variety of cancers. Detected in uterine myometrium.
 CC -1- SIMILARITY: Belongs to the CTAG family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; U87459; AAB49693.1; -; mRNA.
 DR EMBL; AJ003149; CAA05908.1; -; mRNA.
 DR EMBL; AF038567; CAA05202.1; -; mRNA.
 DR HGNC; HGNC:2491; CTAG1B.
 DR MIM; 300156; -;
 KW Antigen; Transmembrane.
 FT TRANSMEM 156 172 Potential.
 FT COMPIAS 5 82 Gly-rich.
 SQ SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;

 Query Match 100.0%; Score 64; DB 1; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 ARASGPGGGAPR 12
 DB 51 ARASGPGGGAPR 62

 RESULT 3
 ID Q7LBV4 HUMAN
 AC Q7LBV4; HUMAN PRELIMINARY; PRT; 180 AA.
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
 DE antigen 1-A).
 GN Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21303268;
 RA Galgoczy P., Rosenthal A., Platzer M.;
 RT "Human-mouse comparative sequence analysis of the NEMO gene reveals an
 RT alternative promoter within the neighboring G6PD gene.";
 RL Gene 271:93-98(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21566154; PubMed=11709543; DOI=10.1093/hmg/10.22.2557;
 RA Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
 RA Patlan H., Ciccodicola A., Kenrick S., Platzer M., D'Urso M.,

RA Nelson D.L.;
 RT "Multiple pathogenic and benign genomic rearrangements occur at a 35
 RT kb duplication involving the NEMO and LAGE2 genes.";
 RL Hum. Mol. Genet. 10:2557-2567(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Platzer M.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Platzer M.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA Galgoczy P., Platzer M.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99454989; PubMed=10523621;
 RA De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
 RT "DNA methylation is the primary silencing mechanism for a set of germ
 RT line- and tumor-specific genes with a CpG-rich promoter.";
 RL Mol. Cell. Biol. 19:7327-7335(1999).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RA Lethe B.G.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF277315; AAL27014.1; -; Genomic DNA.
 DR EMBL; AJ279577; CAB76943.1; -; Genomic DNA.
 DR EMBL; AF277315; AAL27013.1; -; Genomic DNA.
 SQ SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;

 Query Match 100.0%; Score 64; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 ARASGPGGGAPR 12
 DB 51 ARASGPGGGAPR 62

 RESULT 4
 ID CTAG2 HUMAN
 AC O75638; O75637; Q9BU80; Q9UJ89; Q9Y479;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
 GN Name=CTAG2; Synonyms=ESO2, LAGE1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B).
 RC TISSUE=Melanoma;
 RX MEDLINE=98289662; PubMed=9626360;
 RA Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
 RA de Plaen E., Boon T.;
 RT "LAGE-1, a new gene with tumor specificity.";
 RL Int. J. Cancer 76:903-908(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B), AND VARIANTS
 RP GLN-6; GLN-89 AND ARG-138.
 RC TISSUE=Melanoma;
 RX MEDLINE=99325550; PubMed=10399963;
 RA Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
 RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
 RT unexpected translation product of LAGE-1.";
 RL Int. J. Cancer 82:442-448(1999).
 RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LAGE-1B), AND VARIANT
 RC ARG-138.
 RX TISSUE=Placenta;
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L.J., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carlinci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=LAGE-1B; Synonyms=LAGE-1L;
 CC IsoId=O75638-1; Sequence=displayed;
 CC Name=LAGE-1A; Synonyms=LAGE-1S;
 CC IsoId=O75638-2; Sequence=VSP_004301;
 CC -1- TISSUE SPECIFICITY: Testis and very low level in placenta and in
 CC some uterus samples. Observed in 25-50% of tumor samples of
 CC melanomas, non-small-cell lung carcinomas, bladder, prostate and
 CC head and neck cancers.
 CC -1- DOMAIN: A transmembrane domain is present in isoform LAGE-1A.
 CC -1- SIMILARITY: Belongs to the CTAG family.
 CC -----
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 CC -----
 CC EMBL; AJ223093; CAA11117.1; -; Genomic DNA.
 CC EMBL; AJ223093; CAA11116.1; -; Genomic DNA.
 CC EMBL; AJ223040; CAA11043.1; -; mRNA.
 CC EMBL; AJ223041; CAA11044.1; -; mRNA.
 CC EMBL; AJ012834; CAA10194.1; -; mRNA.
 CC EMBL; AJ012835; CAA10196.1; -; mRNA.
 CC EMBL; BC002833; AAH02833.1; -; mRNA.
 CC EMBL; ENSG0000126890; Homo sapiens.
 CC HGNC; HGNC:2492; CTAG2.
 CC H-InvDB; HIX0017163; -.
 CC MIM; 300396; -.
 CC KW Alternative splicing; Antigen; Polymorphism; Transmembrane.
 CC COMPBIAS 5 79 Gly-rich.
 CC COMPBIAS 183 188 Poly-Pro.
 CC VARSPLIC 135 210 MSVVDQREGAGRMVVVWGLSGASPEGQKARDLRTPKHV
 FT SEQRPTGPPGPGAGGDCGCGVAFNVMSFAPHI -> IR
 FT LTAADHRQLQLSISSCLQLSLMLWITQCFLPVLQAQPSG
 FT QRR (in isoform LAGE-1A).
 FT /FTId=VSP_004301.
 FT VARIANT 6 6 R->Q.
 FT /FTId=VAR_007855.
 FT VARIANT 89 89 E->Q.
 FT /FTId=VAR_007856.
 FT VARIANT 138 138 W->R.
 FT /FTId=VAR_007857.
 FT SEQUENCE 210 AA; 21120 MW; 8BE0EE0AE55E8BE CRC64;
 Query Match 87.5%; Score 56; DB 1; Length 210;
 Best Local Similarity 91.7%; Pred. No. 2.8;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARASGPGGAPR 12
 Db 51 ARASGPGGAPR 62
 RESULT 5
 Q63QT8_BURPS PRELIMINARY; PRT; 362 AA.
 ID Q63QT8_BURPS PRELIMINARY;
 AC Q63QT8;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Putative DNA polymerase III.
 GN OrderedLocusNames=BPSL2936;
 OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia; pseudomallei group.
 OX NCBI_TaxID=28450;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K96243;
 RX PubMed=15377794; DOI=10.1073/pnas.0403302101;
 RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
 RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
 RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
 RA Brooks K., Brown K.A., Brown N.P., Challis G.L., Cherevach I.,
 RA Chillingworth T., Cronin A., Crossett B., Davis P., Deshazer D.,
 RA Felwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
 RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
 RA Rabinovitch E., Rutherford K., Sanders M., Simmonds M.,
 RA Songivilai S., Stevens K., Tumapa S., Vesaratchavee M.,
 RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.,
 RT "Genomic plasticity of the causative agent of melioidosis,
 RT Burkholderia pseudomallei.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
 DR EMBL; BX571965; CAH36946.1; -; Genomic DNA.
 DR GO; GO:0003887; F-DNA-directed DNA polymerase activity; IEA.
 DR GO; GO:000260; P-DNA replication; IEA.
 DR InterPro; IPR010372; DNA pol3_delta.
 DR InterPro; IPR005790; DNA pol3_delta.
 DR Pfam; PF06144; DNA pol3_delta; 1.
 DR TIGRFAMs; TIGR01128; hoIA; 1.
 KW Complete proteome.
 SQ SEQUENCE 362 AA; 38726 MW; D5PF3DE783D41E41 CRC64;
 Query Match 84.4%; Score 54; DB 2; Length 362;
 Best Local Similarity 83.3%; Pred. No. 9.3;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARASGPGGAPR 12
 Db 348 ARASGPGGAPR 359
 RESULT 6
 Q62H22_BURMA PRELIMINARY; PRT; 362 AA.
 ID Q62H22_BURMA PRELIMINARY;
 AC Q62H22;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE DNA polymerase III, delta subunit (EC 2.7.7.7).
 GN Name=hoIA; OrderedLocusNames=EMA2451;
 OS Burkholderia mallei (Pseudomonas mallei).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia.
 OX NCBI_TaxID=13373;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 23344;
 RX PubMed=15377793; DOI=10.1073/pnas.0403306101;
 RA Nierman W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E.,

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RA Felblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M., Dodson R.J.,
RA Daugherty S.C., Davidson T.D., Deboy R.T., Dimitrov G., Kolonay J.F.,
RA Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA Madupu R., Mohamoud Y., Nelson W.C., Radune D., Romero C.M.,
RA Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA Zafar N., Zhou L., Fraser C.M.;
RA "Structural flexibility in the Burkholderia mallei genome.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251 (2004).
RL EMBL; CP000010; AAU49707.1; -; Genomic DNA.
CR TIGR; BWA2451; -;
CR GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
CR GO; GO:0016740; P:transferase activity; IEA.
CR GO; GO:0006260; P:DNA replication; IEA.
DR InterPro; IPR010372; DNA pol3_delta.
DR InterPro; IPR005790; DNA polIII_delta.
DR Pfam; PF06144; DNA pol3_delta; 1.
DR TIGRFAMs; TIGR01128; hola; 1.
KW Complete proteome; Nucleotidyltransferase; Transferase.
SQ SEQUENCE 362 AA; 38726 MW; D5FP3DE783D41E41 CRC64;

Query Match 84.4%; Score 54; DB 2; Length 362;
Best Local Similarity 83.3%; Pred. No. 9.3;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
DB 348 ARAAGGGDAPR 359

RESULT 7
Q96BU2 HUMAN
ID Q96BU2 HUMAN PRELIMINARY; PRT; 194 AA.
AC Q96BU2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PLEKHG2 protein (Fragment).
GN Name=PLEKHG2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Schenker C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pancreas;
RA Director MGC Project;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015174; AAH15174.1; -; mRNA.
SQ SEQUENCE 896 AA; 94247 MW; 0DE6869BCFD4C471 CRC64;

Query Match 78.1%; Score 50; DB 2; Length 896;
Best Local Similarity 81.8%; Pred. No. 84;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARASGPGGGAP 11
DB 801 ARROQPGGGAP 811

RESULT 9
Q6DHV6 HUMAN
ID Q6DHV6 HUMAN PRELIMINARY; PRT; 1253 AA.
AC Q6DHV6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DR EMBL; BC015174; AAH15174.1; -; mRNA.

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FT NON TER 1
SQ SEQUENCE 194 AA; 19957 MW; 91AB4FF8F05CBD3C CRC64;

Query Match 78.1%; Score 50; DB 2; Length 194;
Best Local Similarity 81.8%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARASGPGGGAP 11
DB 99 ARROQPGGGAP 109

RESULT 8
Q96D18 HUMAN
ID Q96D18 HUMAN PRELIMINARY; PRT; 896 AA.
AC Q96D18;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PLEKHG2 protein.
GN Name=PLEKHG2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Schenker C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pancreas;
RA Director MGC Project;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013426; AAH13426.1; -; mRNA.
SQ SEQUENCE 896 AA; 94247 MW; 0DE6869BCFD4C471 CRC64;

Query Match 78.1%; Score 50; DB 2; Length 896;
Best Local Similarity 81.8%; Pred. No. 84;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARASGPGGGAP 11
DB 801 ARROQPGGGAP 811

RESULT 9
Q6DHV6 HUMAN
ID Q6DHV6 HUMAN PRELIMINARY; PRT; 1253 AA.
AC Q6DHV6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DR EMBL; BC015174; AAH15174.1; -; mRNA.

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DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE PLEKHG2 protein (Fragment).
GN Name=PLEKHG2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Pancras;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieff P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Pancras;
RC Director MGC Project;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 PH domain.
DR EMBL: BC075858; AAH75858.1; -; mRNA.
DR InterPro: IPR001849; PH.
DR InterPro: IPR000219; RhoGEF.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00621; RhoGEF; 1.
DR SMART: SM00233; PH; 1.
DR SMART: SM00325; RhoGEF; 1.
DR PROSITE: PS00010; DH_2; 1.
DR PROSITE: PS50003; PH_DOMAIN; 1.
FT NON TER 1
FT SEQUENCE 1253; AA; 134404 MW; 534EB31283E535C5 CRC64;

Query Match 78.1%; Score 50; DB 2; Length 1253;
Best Local Similarity 81.8%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARASGPGGGAP 11
DB 1158 ARRGPGGGAP 1168

RESULT 10
Q9H7P9_HUMAN PRELIMINARY; PRT; 1430 AA.
AC Q9H7P9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE FLJ00018 protein (Fragment).
GN Name=PLEKHG2; Synonyms=FLJ00018;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
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RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Spleen;
RX PubMed=14702039; DOI=10.1038/ngl1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata S., Watanabe M., Hiraoaka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hota T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togliya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Inose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshihawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Hishigaki S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Yamagaki M., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamaguchi M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiiwa T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Komatsu T.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45 (2004).
CC -1- SIMILARITY: Contains 1 PH domain.
DR EMBL: AK024429; BAB15719.1; -; mRNA.
DR HSSP: Q64096; 1KZ7.
DR Ensembl: ENSG00000090924; Homo sapiens.
DR HGNC: HGNC:29515; PLEKHG2.
DR InterPro: IPR001849; PH.
DR InterPro: IPR000219; RhoGEF.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00621; RhoGEF; 1.
DR SMART: SM00233; PH; 1.
DR SMART: SM00325; RhoGEF; 1.
DR PROSITE: PS50010; DH_2; 1.
DR PROSITE: PS50003; PH_DOMAIN; 1.
FT NON TER 1
FT SEQUENCE 1430 AA; 152528 MW; E4DF0BFDAACCB6A30 CRC64;

Query Match 78.1%; Score 50; DB 2; Length 1430;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARASGPGGGAP 11
DB 1335 ARRGPGGGAP 1345

RESULT 11
Q5Z8E2_ORYSA PRELIMINARY; PRT; 262 AA.
AC Q5Z8E2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein P0487E11.17.
GN Name=P0487E11.17;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
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OX NCBI_TaxID=39947;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
FX MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayaishi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Ito S., Ito T., Ito Y., Ito Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwana H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y.,
RA Yano M., Jiang J., Gojobori T.;
XT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
RL EMBL; AP003793; BAD53925.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 262 AA; 27141 MW; 816A1189E43BA42A CRC64;

Query Match 75.0%; Score 48; DB 2; Length 262;
Best Local Similarity 83.3%; Pred. No. 50;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
Db 225 ARASGPGGGADR 236

RESULT 12
Q96S27 HUMAN
ID Q96S27 HUMAN PRELIMINARY; PRT; 321 AA.
AC Q96S27;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein gene X.
GN Name=Gene X;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21096910; PubMed=11157797; DOI=10.1093/hmg/10.4.339;
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K., J.,
RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA Higgs D.R.;
RT "Sequence, structure and pathology of the fully annotated terminal 2
RT Mb of the short arm of human chromosome 16.";
RL Hum. Mol. Genet. 10:339-352(2001).
RL EMBL; AB008463; AAK61225.1; -; Genomic_DNA.
DR Ensembl; ENSG00000167933; Homo sapiens.
KW Hypothetical protein.
SQ SEQUENCE 321 AA; 32979 MW; 9C8764CFA17F4CD4 CRC64;

Query Match 75.0%; Score 48; DB 2; Length 321;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
Db 6 ARASGPGGGAR 17

RESULT 13
Q7F1E3 ORYSA
ID Q7F1E3 ORYSA PRELIMINARY; PRT; 449 AA.

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AC Q7F1E3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein OJ1191_A10.131 (Hypothetical protein
DE OJ1014_E06.5).
GN Name=OJ1191_A10.131; Synonyms=OJ1014_E06.5;
OS Oryza sativa [japonica cultivar-group].
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
NCBI_TaxID=39947;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AP003857; BAD08744.1; -; Genomic_DNA.
DR EMBL; AP003888; BAD11573.1; -; Genomic_DNA.
DR Gramene; Q7F1E3; -;
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR008700; NOI.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF05627; NOI; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 449 AA; 47196 MW; B8EFF7708B292296 CRC64;

Query Match 75.0%; Score 48; DB 2; Length 449;
Best Local Similarity 75.0%; Pred. No. 84;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
Db 156 SRASGPGGGAPR 167

RESULT 14
Q6AV33 ORYSA
ID Q6AV33 ORYSA PRELIMINARY; PRT; 367 AA.
AC Q6AV33;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein OSUNBa0063J18.9.
GN Name=OSUNBa0063J18.9;
OS Oryza sativa [japonica cultivar-group].
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
NCBI_TaxID=39947;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Padrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feidblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSUNBa0063J18 genomic sequence.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]_
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC107206; AAT77052.1; -; Genomic_DNA.

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DR Gramene; Q6AV33; --
KW Hypothetical protein.
SQ SEQUENCE 367 AA; 37474 MW; B8C62D9D4CC18C86 CRC64;

Query Match 73.4%; Score 47; DB 2; Length 367;
Best Local Similarity 75.0%; Pred.No. 96;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
   |||||
Db 92 AAASGPGGGGAR 103

RESULT 15
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ID Q4NUK4_9DELT PRELIMINARY; PRT; 895 AA.
AC Q4NUK4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Lga.
OS ORFNames=AdehDRAFT_2813;
GN Anaeromyxobacter dehalogenans 2CP-C.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
OX NCBI_TaxID=290397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P., Richardson P.,
RT "Sequencing of the draft genome assembly of Anaeromyxobacter
RT dehalogenans 2CP-C.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Anaeromyxobacter
RT dehalogenans 2CP-C.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHD0100013; EAL79351.1; -; Genomic DNA.
SQ SEQUENCE 895 AA; 93871 MW; 0AE25B8BF172BDB0 CRC64;

Query Match 73.4%; Score 47; DB 2; Length 895;
Best Local Similarity 81.8%; Pred.No. 2.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RASGPGGGAPR 12
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Db 799 RARGAGGGAPR 809
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Search completed: March 13, 2006, 19:14:28
Job time : 88.1059 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:14:49 ; Search time 22.3059 Seconds
(without alignments)
44.477 Million cell updates/sec

Title: US-09-529-206E-29
Perfect score: 64
Sequence: 1 ARASGFGGAPR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/6 COMB.pap:*
3: /cgn2_6/ptodata/1/iaa/H COMB.pap:*
4: /cgn2_6/ptodata/1/iaa/PTCUS COMB.pap:*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pap:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	180	1	US-08-791-495-9
2	64	100.0	180	2	US-08-937-263B-8
3	64	100.0	180	2	US-09-751-798-8
4	64	100.0	180	2	US-09-392-714-25
5	64	100.0	180	2	US-09-165-546D-15
6	64	100.0	180	2	US-09-341-829A-9
7	64	100.0	180	2	US-09-849-602-30
8	56	87.5	180	1	US-08-791-495-7
9	56	87.5	180	2	US-09-341-829A-7
10	56	87.5	210	1	US-08-791-495-5
11	56	87.5	210	2	US-09-341-829A-5
12	48	75.0	9	2	US-09-344-040C-117
13	48	75.0	9	2	US-09-833-039A-117
14	48	75.0	809	2	US-09-252-991A-11759
15	46	71.9	143	2	US-08-789-329C-10
16	46	71.9	160	2	US-09-252-991A-17249
17	46	71.9	172	2	US-08-789-329C-7
18	46	71.9	175	2	US-08-789-329C-3
19	46	71.9	210	2	US-09-252-991A-24923
20	45	70.3	416	2	US-09-252-991A-30219
21	45	70.3	421	2	US-09-252-991A-32326
22	45	70.3	1427	2	US-10-104-047-3295
23	45	70.3	1427	2	US-09-252-991A-20577
24	44	68.8	196	2	US-09-252-991A-30527
25	44	68.8	456	2	US-09-252-991A-17335
26	44	68.8	679	2	US-09-252-991A-17111
27	43	67.2	324	2	US-09-902-540-11047

28	43	67.2	1228	2	US-09-252-991A-17764	Sequence 17764, A
29	42	65.6	163	2	US-09-252-991A-29111	Sequence 29111, A
30	42	65.6	283	2	US-09-252-991A-17831	Sequence 17831, A
31	42	65.6	505	1	US-08-660-765A-2	Sequence 2, Appli
32	42	65.6	789	2	US-09-252-991A-25611	Sequence 25611, A
33	42	65.6	836	2	US-09-491-356C-21	Sequence 21, Appl
34	41.5	64.8	268	2	US-09-252-991A-31279	Sequence 31279, A
35	41	64.1	177	2	US-09-252-991A-18782	Sequence 18782, A
36	41	64.1	187	2	US-09-252-991A-29442	Sequence 29442, A
37	41	64.1	224	2	US-09-252-991A-30723	Sequence 30723, A
38	41	64.1	310	2	US-09-252-991A-19986	Sequence 19986, A
39	41	64.1	340	2	US-09-949-002-562	Sequence 562, App
40	41	64.1	412	1	US-08-878-989-6	Sequence 6, Appli
41	41	64.1	412	2	US-09-272-796-6	Sequence 6, Appli
42	41	64.1	438	2	US-09-949-016-7812	Sequence 7812, Ap
43	41	64.1	459	1	US-08-630-592-2	Sequence 2, Appli
44	41	64.1	459	1	US-08-714-991-2	Sequence 2, Appli
45	41	64.1	459	2	US-09-032-365A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-495-9

Query Match 100.0%; Score 64; DB 1; Length 180;

Best Local Similarity 100.0%; Pred. No. 0.21; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0;

QY 1 ARASGFGGAPR 12
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Db 51 ARASGFGGAPR 62

RESULT 2
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tsang; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-08-937-263B-8
Query Match 100.0%; Score 64; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.21; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARASPGGGGAPR 12
DB 51 ARASPGGGGAPR 62
RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tsang; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York

COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6525177man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 180
TYPE: amino acid
TOPOLOGY: linear
US-09-751-798-8
Query Match 100.0%; Score 64; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.21; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARASPGGGGAPR 12
DB 51 ARASPGGGGAPR 62
RESULT 4
US-09-392-714-25
; Sequence 25, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tsang
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-392-714-25
Query Match 100.0%; Score 64; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.21; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARASPGGGGAPR 12
DB 51 ARASPGGGGAPR 62

RESULT 5
US-09-165-546D-15
; Sequence 15, Application US/09165546D
; Patent No. 6723832
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
; USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546D
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6723832man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15

Query Match 100.0%; Score 64; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.21; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0;

Qy 1 ARASGPGGGAPR 12
| | | | | | | | | | | | | |
Db 51 ARASGPGGGAPR 62

RESULT 6
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; <151> 1997-01-27

; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-9

Query Match 100.0%; Score 64; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.21; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0;

Qy 1 ARASGPGGGAPR 12
| | | | | | | | | | | | | |
Db 51 ARASGPGGGAPR 62

RESULT 7
US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseeng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30

Query Match 100.0%; Score 64; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.21; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0;

Qy 1 ARASGPGGGAPR 12
| | | | | | | | | | | | | |
Db 51 ARASGPGGGAPR 62

RESULT 8
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth , Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-7

Query Match      87.5%; Score 56; DB 1; Length 180;
Best Local Similarity 91.7%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 ARASGPGGGAPR 12
      ||||| |||||
Db      51 ARASGPRGGAPR 62

RESULT 9
US-09-341-829A-7
; Sequence 7, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-7

Query Match      87.5%; Score 56; DB 2; Length 180;
Best Local Similarity 91.7%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 ARASGPGGGAPR 12
      ||||| |||||
Db      51 ARASGPRGGAPR 62

RESULT 10
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-5

Query Match      87.5%; Score 56; DB 1; Length 210;
Best Local Similarity 91.7%; Pred. No. 2.7;
Matches 11; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 ARASGPGGGAPR 12
      ||||| |||||
Db      51 ARASGPRGGAPR 62

RESULT 11
US-09-341-829A-5
; Sequence 5, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-5

Query Match      87.5%; Score 56; DB 2; Length 210;
Best Local Similarity 91.7%; Pred. No. 2.7;
Matches 11; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 ARASGPGGGAPR 12
      ||||| |||||
Db      51 ARASGPRGGAPR 62

RESULT 12

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US-09-344-040C-117
; Sequence 117, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 117
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-117

Query Match 75.0%; Score 48; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RASGPGGGA 10
|||||
Db 1 RASGPGGGA 9

RESULT 13
US-09-833-039A-117
; Sequence 117, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 117
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-117

Query Match 75.0%; Score 48; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RASGPGGGA 10
|||||
Db 1 RASGPGGGA 9

RESULT 14
US-09-252-991A-31759
; Sequence 31759, Application US/09252991A

; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31759
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31759

Query Match 75.0%; Score 48; DB 2; Length 809;
Best Local Similarity 81.8%; Pred. No. 97;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RASGPGGAPR 12
|||||
Db 244 RAGGPRGGAPR 254

RESULT 15
US-08-789-329C-10
; Sequence 10, Application US/08789329C
; Patent No. 6165755
; GENERAL INFORMATION:
; APPLICANT: SHERWOOD ET AL.
; TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL
; TITLE OF INVENTION: FOR IMPROVED POULTRY PRODUCTION
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204-2988
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: WordPerfect 7.0 & ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,329C
; FILING DATE: 01/23/97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Earp, David J.
; REGISTRATION NUMBER: 41,401
; REFERENCE/DOCKET NUMBER: 2847-46468/DJE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 143 aa
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-789-329C-10

Query Match 71.9%; Score 46; DB 2; Length 143;
Best Local Similarity 72.7%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 2 RASGPGGGAPR 12
|||
Db 56 RAGAPGGGGPR 66
|||

Search completed: March 13, 2006, 19:18:52
Job time : 23.3059 secs

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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:51:56 ; Search time 72.5647 Seconds
(without alignments)
69.096 Million cell updates/sec

Title: US-09-529-206E-29
Perfect score: 64
Sequence: 1 ARASGPGGAPR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pap.*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	30	4	US-10-296-734-1404
2	64	100.0	179	5	US-10-482-029-202
3	64	100.0	180	3	US-09-751-798-8
4	64	100.0	180	3	US-09-849-602-30
5	64	100.0	180	4	US-10-023-182-8
6	64	100.0	180	4	US-10-207-655-71
7	64	100.0	180	4	US-10-364-614-14
8	64	100.0	180	4	US-10-026-066-3
9	64	100.0	180	4	US-10-117-937-74
10	64	100.0	180	4	US-10-295-027-386
11	64	100.0	180	4	US-10-296-734-832
12	64	100.0	180	4	US-10-188-832-139
13	64	100.0	180	4	US-10-777-053-11
14	64	100.0	180	4	US-10-751-088-15
15	64	100.0	180	4	US-10-657-022-74
16	64	100.0	180	4	US-10-837-217-11
17	64	100.0	180	5	US-10-877-373-9
18	64	100.0	180	5	US-10-723-860-1270
19	64	100.0	180	5	US-10-871-708-7
20	64	100.0	180	5	US-10-895-523-3
21	64	100.0	180	5	US-10-182-506A-3
22	64	100.0	180	5	US-10-756-149-5024
23	64	100.0	180	6	US-11-067-064-74
24	64	100.0	180	6	US-11-067-159-74
25	64	100.0	397	3	US-09-821-883-27
26	64	100.0	397	6	US-11-144-912-27
27	64	100.0	3541	4	US-10-296-734-1454

28	56	87.5	30	4	US-10-296-734-1436	Sequence 1436, Ap
29	56	87.5	135	4	US-10-295-027-388	Sequence 388, App
30	56	87.5	135	4	US-10-188-832-141	Sequence 141, Appl
31	56	87.5	180	4	US-10-146-473-69	Sequence 69, Appl
32	56	87.5	180	4	US-10-117-937-75	Sequence 75, Appl
33	56	87.5	180	4	US-10-296-734-834	Sequence 834, App
34	56	87.5	180	4	US-10-468-406-4	Sequence 4, Appli
35	56	87.5	180	4	US-10-657-022-75	Sequence 75, Appli
36	56	87.5	180	5	US-10-877-373-7	Sequence 7, Appli
37	56	87.5	180	6	US-11-067-064-75	Sequence 75, Appl
38	56	87.5	180	6	US-11-067-159-75	Sequence 75, Appl
39	56	87.5	210	4	US-10-157-031-88	Sequence 88, Appl
40	56	87.5	210	4	US-10-117-937-76	Sequence 76, Appl
41	56	87.5	210	5	US-10-657-022-76	Sequence 76, Appl
42	56	87.5	210	5	US-10-877-373-5	Sequence 5, Appli
43	56	87.5	210	6	US-11-067-064-76	Sequence 76, Appl
44	56	87.5	210	6	US-11-067-159-76	Sequence 76, Appl
45	55	85.9	10	4	US-10-447-161-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-10-296-734-1404
; Sequence 1404, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1404
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA segment 4
US-10-296-734-1404

Query Match 100.0%; Score 64; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARASGPGGAPR 12
DB 8 ARASGPGGAPR 19

RESULT 2
US-10-482-029-202
; Sequence 202, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-202

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Query Match      100.0%; Score 64; DB 5; Length 179;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ARASGPGGGAPR 12
      |||||
Db      51 ARASGPGGGAPR 62

RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. US20020010321A1
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. US20020010321A1man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-09-751-798-8

Query Match      100.0%; Score 64; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ARASGPGGGAPR 12
      |||||
Db      51 ARASGPGGGAPR 62

RESULT 4
US-09-849-602-30
; Sequence 30, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
```



```
Query Match      100.0%; Score 64; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ARASGPGGGAPR 12
Db      51 ARASGPGGGAPR 62

RESULT 6
US-10-207-655-71
; Sequence 71, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-71

Query Match      100.0%; Score 64; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ARASGPGGGAPR 12
Db      51 ARASGPGGGAPR 62

RESULT 7
US-10-364-614-14
; Sequence 14, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
; APPLICANT: JAGER, Elke
; APPLICANT: KNUTH, Alexander
; APPLICANT: OLD, Lloyd
; APPLICANT: Gnjatic, Sacha
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
; FILE REFERENCE: LUD 5726.1 CIP
; CURRENT APPLICATION NUMBER: US/10/364,614
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/355,828
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-614-14

Query Match      100.0%; Score 64; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ARASGPGGGAPR 12
Db      51 ARASGPGGGAPR 62

RESULT 8
US-10-026-066-3
; Sequence 3, Application US/10026066
; Publication No. US20030215425A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
; TITLE OF INVENTION: PRESENTING CELLS
; FILE REFERENCE: CTLMIM.21CPI
; CURRENT APPLICATION NUMBER: US/10/026,066
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-026-066-3

Query Match      100.0%; Score 64; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ARASGPGGGAPR 12
Db      51 ARASGPGGGAPR 62

RESULT 9
US-10-117-937-74
; Sequence 74, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLMIM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-74

Query Match      100.0%; Score 64; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ARASGPGGGAPR 12
Db      51 ARASGPGGGAPR 62

RESULT 10
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US-10-295-027-386
; Sequence 386, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 386
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-386

Query Match 100.0%; Score 64; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
Db 51 ARASGPGGGAPR 62

RESULT 11
US-10-296-734-832
; Sequence 832, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU P07761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 832

US-10-295-027-386
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYNSOla consensus polypeptide
US-10-296-734-832

Query Match 100.0%; Score 64; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
Db 51 ARASGPGGGAPR 62

RESULT 12
US-10-188-832-139
; Sequence 139, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-139

Query Match 100.0%; Score 64; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
Db 51 ARASGPGGGAPR 62

RESULT 13
US-10-777-053-11
; Sequence 11, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: MANK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
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: PRIOR APPLICATION NUMBER: 60/336, 968
: PRIOR FILING DATE: 2001-11-07
: NUMBER OF SEQ ID NOS: 979
: SOFTWARE: FASTSEQ for Windows Version
: SEQ ID NO 11
: LENGTH: 180
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-777-053-11

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Query Match 100.0%; Score 64; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 12; Conservative 0; Mismatches 0; Indels

Qy 1 ARASGPGGGAPR 12
Db 51 ARASGPGGGAPR 62

RESULT 14
US-10-751-088-15 ;
; Sequence 15, Application US/10751088
; Publication No. US20040158044A1
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NT-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
; USES THEREOF

Query Match 100.0%; Score 64; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 12; Conservative 0; Mismatches 0; Indels

QY 1 ARASGPGGGAPR 12
Db 51 ARASGPGGGAPR 62

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RESULT 15
US-10-657-022-74
; Sequence 74, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPIOTOPE SEQUENCES
; FILE REFERENCE: MANKK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-657-022-74

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Query Match 100.0%; Score 64; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARASGPGGAPR 12
Db 51 ARASGPGGAPR 62

Search completed: March 13, 2006, 20:02:27
Job time : 72.5647 secs

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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:54:06 ; Search time 8.18824 Seconds
(without alignments)
40.793 Million cell updates/sec

Title: US-09-529-206E-29
Perfect score: 64
Sequence: 1 ARASGPGGAPR 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 161667

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	64	100.0	180	7	US-11-155-288-7
2	64	100.0	240	7	US-11-021-441-28
3	52	81.2	20	6	US-10-623-155-496
4	47	73.4	306	7	US-11-096-568A-20556
5	46	71.9	134	7	US-11-096-568A-23806
6	45	70.3	678	7	US-11-072-512-3295
7	44	68.8	558	7	US-11-096-568A-26217
8	43	67.2	353	7	US-11-096-568A-22334
9	43	67.2	358	7	US-11-096-568A-22333
10	43	67.2	413	7	US-11-096-568A-22332
11	43	67.2	420	7	US-11-096-568A-22332
12	41	64.1	365	7	US-11-108-528-58
13	41	64.1	537	7	US-11-179-958A-2
14	41	64.1	555	7	US-11-072-512-3369
15	41	64.1	953	7	US-11-037-243-66
16	40.5	63.3	280	7	US-11-143-980-34
17	40	62.5	379	7	US-11-109-156-16
18	40	62.5	374	6	US-10-531-036-35
19	40	62.5	1832	7	US-11-087-099-7762
20	39	60.9	213	7	US-11-072-512-2722
21	39	60.9	233	7	US-11-240-769-58
22	39	60.9	238	6	US-10-821-234-1240
23	39	60.9	430	6	US-10-992-577-8
24	39	60.9	430	6	US-10-508-892-2
25	39	60.9	430	7	US-11-223-294-54

26	39	60.9	618	7	US-11-078-735-18	Sequence 18, Appl
27	39	60.9	618	7	US-11-050-346-63	Sequence 63, Appl
28	39	60.9	618	7	US-11-103-077-18	Sequence 18, Appl
29	39	60.9	662	7	US-11-072-175-184	Sequence 184, App
30	39	60.9	836	7	US-11-154-227-105	Sequence 105, App
31	39	60.9	904	7	US-11-154-227-97	Sequence 97, Appl
32	38.5	60.2	219	7	US-11-096-568A-1390	Sequence 1390, Ap
33	38	59.4	132	7	US-11-096-568A-14323	Sequence 14323, A
34	38	59.4	162	7	US-11-096-568A-641	Sequence 641, App
35	38	59.4	228	7	US-11-096-568A-16457	Sequence 16457, A
36	38	59.4	235	7	US-11-096-568A-1070	Sequence 1070, Ap
37	38	59.4	236	7	US-11-096-568A-22845	Sequence 22845, A
38	38	59.4	249	7	US-11-096-568A-23045	Sequence 23045, A
39	38	59.4	274	7	US-11-096-568A-22603	Sequence 22603, A
40	38	59.4	306	7	US-11-096-568A-12071	Sequence 12071, A
41	38	59.4	320	7	US-11-096-568A-988	Sequence 988, App
42	38	59.4	341	6	US-10-821-234-1628	Sequence 1628, Ap
43	38	59.4	438	6	US-10-650-3269-9	Sequence 9, Appli
44	38	59.4	459	7	US-11-096-568A-21887	Sequence 21887, A
45	38	59.4	830	6	US-10-921-793-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1

US-11-155-288-7
; Sequence 7, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J. L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.050A
; CURRENT APPLICATION NUMBER: US/11/155,288
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-7

Query Match 100.0%; Score 64; DB 7; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARASGPGGAPR 12
DB 51 ARASGPGGAPR 62

RESULT 2

US-11-021-441-28
; Sequence 28, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THERSOF
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06

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; PRIOR APPLICATION NUMBER: US 60/615,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/23881
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein
US-11-021-441-28

Query Match          100.0%; Score 64; DB 7; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARASGPGGAPR 12
Db 111 ARASGPGGAPR 122

RESULT 3
US-10-623-155-496
; Sequence 496, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fangeef, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 496
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-496

Query Match          81.2%; Score 52; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARASGPGGGA 10
Db 11 ARASGPGGGA 20

RESULT 4
US-11-096-568A-20556
; Sequence 20556, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20556
```

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;
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(306)
; OTHER INFORMATION: Ceres Seq. ID no. 12383286
US-11-096-568A-20556

Query Match          73.4%; Score 47; DB 7; Length 306;
Best Local Similarity 81.8%; Pred. No. 9.5;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARASGPGGGAP 11
Db 91 ARADPGGTGAP 101

RESULT 5
US-11-096-568A-23806
; Sequence 23806, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23806
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(134)
; OTHER INFORMATION: Ceres Seq. ID no. 12415289
US-11-096-568A-23806

Query Match          71.9%; Score 46; DB 7; Length 134;
Best Local Similarity 72.7%; Pred. No. 6.4;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARASGPGGGAP 11
Db 69 ARGAGPGGAGAP 79

RESULT 6
US-11-072-512-3295
; Sequence 3295, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
```

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; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3295
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3295

Query Match 70.3%; Score 45; DB 7; Length 678;
Best Local Similarity 80.0%; Pred. No. 35;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RASGPGGGAP 11
Db 592 RAAGPGGGWP 601

RESULT 7
US-11-096-568A-26217
; Sequence 26217, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26217
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(558)
; OTHER INFORMATION: Ceres Seq. ID no. 13498878
US-11-096-568A-26217

Query Match 68.8%; Score 44; DB 7; Length 558;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
Db 389 ARQGPAGGPR 400

RESULT 8
US-11-096-568A-22334
; Sequence 22334, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22334
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (1)..(353)
; OTHER INFORMATION: Ceres Seq. ID no. 12408544
US-11-096-568A-22334

Query Match 67.2%; Score 43; DB 7; Length 353;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
Db 109 ARQGPGEQPR 120

RESULT 9
US-11-096-568A-22333
; Sequence 22333, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22333
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(358)
; OTHER INFORMATION: Ceres Seq. ID no. 12408543
US-11-096-568A-22333

Query Match 67.2%; Score 43; DB 7; Length 358;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
Db 114 ARQGPGEQPR 125

RESULT 10
US-11-096-568A-27265
; Sequence 27265, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27265
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(413)
; OTHER INFORMATION: Ceres Seq. ID no. 15180691
US-11-096-568A-27265

Query Match 67.2%; Score 43; DB 7; Length 413;
Best Local Similarity 72.7%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARASGPGGGAP 11
Db 95 ARRRGPGGAAP 105
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RESULT 11
US-11-096-568A-22332
; Sequence 22332, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 22332
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(420)
; OTHER INFORMATION: Ceres Seq. ID no. 12408542
US-11-096-568A-22332

Query Match 67.2%; Score 43; DB 7; Length 420;
Best Local Similarity 66.7%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ARASGPGGGAPR 12
||| ||| |||
Db 176 ARGQPGGGRPR 187

RESULT 12
US-11-108-528-58
; Sequence 58, Application US/11108528
; Publication No. US20050261189A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Glenn
; APPLICANT: Marvin, Martha
; APPLICANT: Li, Dean Y.
; APPLICANT: Wang, Elizabeth
; APPLICANT: Chen, C. M. Amy
; APPLICANT: Shamah, Steven M.
; TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
; TITLE OF INVENTION: PROLIFERATION
; FILE REFERENCE: HYDR-P01-041
; CURRENT APPLICATION NUMBER: US/11/108,528
; CURRENT FILING DATE: 2005-04-18
; PRIOR FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,137
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/598,368
; PRIOR FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Mouse
US-11-108-528-58

Query Match 64.1%; Score 41; DB 7; Length 365;
Best Local Similarity 80.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RASGPGGGAP 11
||||| |||
Db 273 RASGSGGGDP 282

RESULT 13
US-11-179-958A-2
; Sequence 2, Application US/11179958A

; Publication No. US20060030537A1
; GENERAL INFORMATION:
; APPLICANT: Chalfant, Charles E.
; APPLICANT: Hannun, Yusef A.
; APPLICANT: Pettus, Benjamin J.
; APPLICANT: Bielawska, Alicja
; TITLE OF INVENTION: Ceramide Kinase and Uses Thereof
; FILE REFERENCE: 9175-028-999 (MUSC Ref P0401)
; CURRENT APPLICATION NUMBER: US/11/179,958A
; CURRENT FILING DATE: 2005-07-11
; PRIOR APPLICATION NUMBER: 60/586,909
; PRIOR FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human ceramide kinase
US-11-179-958A-2

Query Match 64.1%; Score 41; DB 7; Length 537;
Best Local Similarity 70.0%; Pred. No. 99;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RASGPGGGAP 11
|: ||| |||
Db 36 RSPGPGAGAP 45

RESULT 14
US-11-072-512-3369
; Sequence 3369, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIG, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3369
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3369

Query Match 64.1%; Score 41; DB 7; Length 555;
Best Local Similarity 77.8%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 ASGPGGGAP 11
|||||:
Db 473 ASGPGGSP 481

RESULT 15
US-11-037-243-66
; Sequence 66, Application US/11037243
; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; PRIOR FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 953
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-66

Query Match 64.1%; Score 41; DB 7; Length 953;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GPGGGAPR 12
|||||
Db 214 GPGGGHPR 221

Search completed: March 13, 2006, 20:03:31
Job time : 8.18824 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 18:52:59 ; Search time 82.8235 Seconds
(without alignments)
58.355 Million cell updates/sec

Title: US-09-529-206E-30
Perfect score: 60
Sequence: 1 RASGPGGAPR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	11	2	AAY06066 Human can
2	60	100.0	12	2	AAY06065 Human can
3	60	100.0	13	2	AAY06064 Human can
4	60	100.0	14	2	AAY05986 Human can
5	60	100.0	15	2	AAY05978 Human can
6	60	100.0	20	2	AAY05979 Human can
7	60	100.0	30	5	AAY05105 Human NYN
8	60	100.0	179	8	ADK68648 Epitope 1
9	60	100.0	180	2	AAY62584 Cancer as
10	60	100.0	180	2	AAY69665 Human NY-
11	60	100.0	180	2	AAY05965 Human can
12	60	100.0	180	3	AAY52430 Human tum
13	60	100.0	180	3	AAY70862 Human tum
14	60	100.0	180	3	AAB03154 Human oes
15	60	100.0	180	4	AAB69946 Human NY-
16	60	100.0	180	4	AAG67164 Amino aci
17	60	100.0	180	4	AAY01535 Human NY-
18	60	100.0	180	4	AAY07714 Human NY
19	60	100.0	180	5	AAY04818 Human NYN
20	60	100.0	180	5	AAY01543 Human tum
21	60	100.0	180	6	ABR58672 Human can
22	60	100.0	180	6	ABR48210 Human bla
23	60	100.0	180	6	ABU56508 Lung can
24	60	100.0	180	6	ABU56694 Lung can

25	60	100.0	180	6	ABP74198 Human NY-
26	60	100.0	180	6	ABU64816 Human NY-
27	60	100.0	180	6	ABR83438 Human NY-
28	60	100.0	180	7	ADC09576 NY-ESO-1
29	60	100.0	180	7	ADD35564 Human NY-
30	60	100.0	180	7	ADD35568 Human NY-
31	60	100.0	180	7	ADD25510 Binding d
32	60	100.0	180	7	ADN39068 Cancer/an
33	60	100.0	180	8	ADJ54139 Human NY-
34	60	100.0	180	8	ADM72815 Human NY-
35	60	100.0	180	8	ADM73418 CAG-3 pro
36	60	100.0	180	8	ADM73417 Human NY-
37	60	100.0	180	8	ADQ18451 Human sof
38	60	100.0	180	8	ADQ10446 Autoimmun
39	60	100.0	180	8	ADS80926 Tumour as
40	60	100.0	180	9	ADW44353 Human aut
41	60	100.0	180	9	ADY85096 Tumor ant
42	60	100.0	180	9	ADZ28913 NY-ESO-1
43	60	100.0	180	9	ADZ42374 Immunogen
44	60	100.0	180	9	AEA35651 Human NY-
45	60	100.0	240	9	ADW99402 NY-ESO-1/

ALIGNMENTS

RESULT 1
AAY06066
ID AAY06066 standard; peptide; 11 AA.
XX
AC AAY06066;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 peptide.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; cytotoxic T lymphocyte; CTL.
XX
OS Homo sapiens.
XX
PN WO9918206-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US019609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang RF, Rosenberg SA;
XX
DR WPI; 1999-277270/23.
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
PS Example 11; Page 50; 88pp; English.
XX
CC This peptide corresponds to amino acid residues 52-62 of human NY ESO-1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is capable of eliciting an antigen specific immune response by T cells.
CC Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,

CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 CC as breast, prostate, ovarian, pancreatic and thyroid cancers

XX Sequence 11 AA;

Query Match 100.0%; Score 60; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.14; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0;

QY 1 RASGPGGGAPR 11

Db 1 RASGPGGGAPR 11

RESULT 2

AAAY06065

ID AAY06065 standard; peptide; 12 AA.

XX AC AAY06065;

ET 16-AUG-1999 (first entry)

DE Human cancer antigen NY ESO-1/CAG-3 peptide.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine; cytotoxic T lymphocyte; CTL.

OS Homo sapiens.

XX WO9918206-A2.

PN 15-APR-1999.

PD 21-SEP-1998; 98WO-US019609.

PF 08-OCT-1997; 97US-0061428P.

PR (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA Wang RF, Rosenberg SA;

PI WPI; 1999-277270/23.

DR Cancer antigen NY ESO1/CAG-3.

XX Example 11; Page 50; 88pp; English.

XX This peptide corresponds to amino acid residues 51-62 of human NY ESO-1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers

XX Sequence 12 AA;

Query Match 100.0%; Score 60; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.15; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0;

QY 1 RASGPGGGAPR 11

Db 2 RASGPGGGAPR 12

RESULT 3

AAAY06064

ID AAY06064 standard; peptide; 13 AA.

XX AC AAY06064;

DT 16-AUG-1999 (first entry)

XX Human cancer antigen NY ESO-1/CAG-3 peptide.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine; cytotoxic T lymphocyte; CTL.

XX Homo sapiens.

XX WO9918206-A2.

XX 15-APR-1999.

XX 21-SEP-1998; 98WO-US019609.

XX 08-OCT-1997; 97US-0061428P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang RF, Rosenberg SA;

XX WPI; 1999-277270/23.

XX Cancer antigen NY ESO1/CAG-3.

XX Example 11; Page 50; 88pp; English.

XX This peptide corresponds to amino acid residues 50-62 of human NY ESO-1/CAG-3 ORF1 (see AAY05965), a new and potent tumour antigen that is capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers

XX Sequence 13 AA;

Query Match 100.0%; Score 60; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.16; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0;

QY 1 RASGPGGGAPR 11

Db 3 RASGPGGGAPR 13

RESULT 4

AAAY05986

ID AAY05986 standard; peptide; 14 AA.

XX AC AAY05986;

DT 16-AUG-1999 (first entry)

XX Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.

KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO9918206-A2.
 XX
 PD 15-APR-1999.
 XX
 XX 21-SEP-1998; 98WO-US019609.
 XX
 XX 08-OCT-1997; 97US-0061428P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Wang RF, Rosenberg SA;
 XX WPI; 1999-277270/23.
 XX
 XX Cancer antigen NY ESO1/CAG-3.
 XX
 XX Claim 25; Page 50; 88pp; English.
 XX
 CC The present sequence represents a cancer peptide that corresponds to
 CC amino acid residues 49-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
 CC AAY05965), a new and potent tumour antigen capable of eliciting an
 CC antigen specific immune response by T cells. Cancer peptides derived from
 CC CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
 CC variants (see AAY05967-87), are useful as cancer vaccines that protect
 CC against cancer. The invention provides: vectors and host cells (also
 CC useful as vaccines); a method of diagnosis of cancer or precancer; a
 CC transgenic animal; antisense oligonucleotides that inhibit expression of
 CC the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
 CC cancer peptide, useful in diagnostic and detection assays; and methods
 CC for preventing or inhibiting cancer by administering a cancer peptide,
 CC with or without an HLA molecule. The cancer peptides form part of, or are
 CC derived from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
 CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
 CC treated by inducing cancer-specific T cells in vitro for subsequent
 CC return to a patient
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 100.0%; Score 60; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASGPGGGAPR 11
 DB 4 RASGPGGGAPR 14
 RESULT 5
 AAY05978
 ID AAY05978 standard; peptide; 15 AA.
 XX
 AC AAY05978;
 XX
 XX 16-AUG-1999 (first entry)
 DT
 DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
 XX
 KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine.

KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO9918206-A2.
 XX
 PD 15-APR-1999.
 XX
 XX 21-SEP-1998; 98WO-US019609.
 XX
 XX 08-OCT-1997; 97US-0061428P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Wang RF, Rosenberg SA;
 XX WPI; 1999-277270/23.
 XX
 XX Cancer antigen NY ESO1/CAG-3.
 XX
 XX Claim 15; Page 64; 88pp; English.
 XX
 CC The present sequence represents a cancer peptide that corresponds to
 CC amino acid residues 48-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
 CC AAY05965), a new and potent tumour antigen capable of eliciting an
 CC antigen specific immune response by T cells. Cancer peptides derived from
 CC CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
 CC variants (see AAY05967-87), are useful as cancer vaccines that protect
 CC against cancer. The invention provides: vectors and host cells (also
 CC useful as vaccines); a method of diagnosis of cancer or precancer; a
 CC transgenic animal; antisense oligonucleotides that inhibit expression of
 CC the cancer peptide or tumour antigen; antibodies reacting with a CAG-3
 CC cancer peptide, useful in diagnostic and detection assays; and methods
 CC for preventing or inhibiting cancer by administering a cancer peptide,
 CC with or without an HLA molecule. The cancer peptides form part of, or are
 CC derived from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
 CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
 CC treated by inducing cancer-specific T cells in vitro for subsequent
 CC return to a patient
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 100.0%; Score 60; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASGPGGGAPR 11
 DB 5 RASGPGGGAPR 15
 RESULT 6
 AAY05979
 ID AAY05979 standard; peptide; 20 AA.
 XX
 AC AAY05979;
 XX
 XX 16-AUG-1999 (first entry)
 DT
 DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.
 XX
 KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine.

```

OS Homo sapiens.
XX Synthetic.
XX WO918206-A2.
XX PD 15-APR-1999.
XX XX
XX 21-SEP-1998; 98WO-US019609.
XX XX
XX 08-OCT-1997; 97US-0061428P.
XX XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA
XX Wang RF, Rosenberg SA;
XX XX
XX WPI; 1999-277270/23.
XX DR
XX Cancer antigen NY ESO1/CAG-3.
XX FT
XX Claim 16; Page 64; 89pp; English.
XX XX
XX The present sequence represents a cancer peptide that is based on amino
XX acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AA05965),
XX a new and potent tumour antigen capable of eliciting an antigen specific
XX immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-
XX 3 ORF2 (see AA05966), portions of them and their variants (see AA05967-
XX 87), are useful as cancer vaccines that protect against cancer. The
XX invention provides: vectors and host cells (also useful as vaccines); a
XX method of diagnosis of cancer or precancer; a transgenic animal;
XX antisense oligonucleotides that inhibit expression of the cancer peptide
XX or tumour antigen; antibodies reacting with a CAG-3 cancer peptide,
XX useful in diagnostic and detection assays; and methods for preventing or
XX inhibiting cancer by administering a cancer peptide, with or without an
XX HLA molecule. The cancer peptides form part of, or are derived from,
XX cancers such as primary or metastatic melanoma, thymoma, lymphoma,
XX sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
XX cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
XX prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by
XX inducing cancer-specific T cells in vitro for subsequent return to a
XX patient
XX XX
XX Sequence 20 AA;
SQ
Query Match 100.0%; Score 60; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASGPGGGAPR 11
DB |||||
10 RASGPGGGAPR 20
RESULT 7
AAU85105
ID AAU85105 standard; peptide; 30 AA.
XX AC
XX AAU85105;
XX XX
XX 08-MAY-2002 (first entry)
XX DT
XX Human NYNSO1a segment 4.
XX DE
XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
XX KW viral infection; human immunodeficiency virus; melanoma;
XX KW bacterial infection; Salmonella; Legionella; parasitic infection;
XX KW Trypanosoma; Toxoplasma; Giardia.
XX XX
XX Homo sapiens.
XX OS
XX WO200190197-A1.
XX PN
XX 29-NOV-2001.
XX PD
XX XX

PF 25-MAY-2001; 2001WO-AU000622.
XX XX
XX 26-MAY-2000; 2000AU-00007761.
XX PR
XX (AUSU ) UNIV AUSTRALIAN NAT.
XX PA
XX Thomson SA, Ramshaw IA;
XX PI
XX WPI; 2002-147575/19.
XX DR
XX N-PSDB; ABK36925.
XX XX
XX New synthetic polypeptides having several different segments of at least
XX one parent polypeptide linked together differently compared to the
XX linkage in the parent polypeptide, for inducing immune response against a
XX pathogen or cancer.
XX PT
XX Example 3; Fig 27; 364pp; English.
XX PS
XX The invention relates to a new synthetic polypeptide (I) comprising
XX several different segments of at least one parent polypeptide linked
XX together in a different relationship relative to their linkage in the
XX parent polypeptide to impede, abrogate or otherwise alter at least one
XX function associated with the parent polypeptide and for inducing an
XX immune response against a pathogen or cancer. Also included are a
XX synthetic polynucleotide encoding and a computer system for designing the
XX synthetic polypeptides. The synthetic polypeptides and polynucleotides
XX are referred to as a Savine. The synthetic polypeptide is useful for
XX modulating immune responses preferably directed against a pathogen or a
XX cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
XX and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
XX oesophagus, brain, testicle, uterus), as potentiating agents.
XX Compositions comprising the polypeptide may be used in the treatment or
XX prophylaxis against viral (such as infections caused by HIV (human
XX immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
XX virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
XX (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
XX Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
XX (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
XX Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
XX a peptide derived from a parent protein used to construct a savine of the
XX invention
XX XX
XX Sequence 30 AA;
SQ
Query Match 100.0%; Score 60; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASGPGGGAPR 11
DB |||||
9 RASGPGGGAPR 19
RESULT 8
ADK68648
ID ADK68648 standard; protein; 179 AA.
XX AC
XX ADK68648;
XX XX
XX 06-MAY-2004 (first entry)
XX DT
XX Epitope liberation-related NY-ESO-1 protein SeqID11.
XX DE
XX epitope liberation; substrate; proteasome; cytostatic; antibacterial;
XX KW proteoglycan; fungicide; T-cell activator; vaccine; housekeeping epitope;
XX KW cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;
XX KW virus; bacterium; protozoan; fungus; housekeeping proteasome system;
XX human.
XX KW
XX Homo sapiens.
XX OS
XX US2003228634-A1.
XX PN
XX

```

```

PD 11-DEC-2003.
XX
XX
PF 07-NOV-2002; 2002US-00292413.
XX
XX
PR 07-NOV-2001; 2001US-0336968P.
XX
XX (SIMA/) SIMARD U J L.
PA (DIAM/) DIAMOND D C.
PA (QIUZ/) QIU Z.
PA (LEIX/) LEI X.
XX
XX Simard JYL, Diamond DC, Qiu Z, Lei X;
XX
XX WPI; 2004-167209/16.
DR N-PSDB; ADK68674.
XX
XX
XX Identifying polypeptide suitable for epitope e.g., housekeeping epitope,
PT liberation by contacting substrate polypeptide comprising epitope of
PT interest, with proteasome, and assaying for liberation of epitope.
XX
XX Example 2; SEQ ID NO 11; 67pp; English.
XX
XX This invention relates to a novel method of identifying a polypeptide
CC suitable for epitope liberation, including the steps of identifying an
CC epitope of interest; providing substrate polypeptide sequence including
CC the epitope, wherein the substrate permits processing by a proteasome;
CC contacting the substrate with a composition including the proteasome;
CC under conditions that support processing of the substrate by proteasome;
CC and assaying for liberation of epitope. The invention may be useful for
CC the development of compounds with a cytostatic, antibacterial,
CC protozoacide or fungicide activity acting as T-cell activators. In
CC addition, the invention may allow development of a vaccine. The invention
CC is useful for identifying a polypeptide suitable for epitope liberation,
CC where the epitope is a housekeeping epitope. The compositions comprising
CC the identified housekeeping epitopes are useful in vitro in vaccine
CC development or in the generation or expansion of cytotoxic T lymphocyte
CC (CTL) to be used in adoptive immunotherapy. The invention is also useful
CC for activating T-cells against neoplastic cells, and cells infected with
CC virus, bacterium, protozoan or fungus. CTL epitopes are identified based
CC on the knowledge that such epitopes are, in fact, produced by the
CC housekeeping proteasome system. Once identified, these epitopes, embodied
CC as peptides, can be used to successfully immunise or induce therapeutic
CC CTL responses against housekeeping proteasome expressing target cells in
CC the host. The present sequence is that of a protein which is related to
CC the method of the invention.
XX
XX Sequence 179 AA;
SQ
Query Match 100.0%; Score 60; DB 8; Length 179;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGGAPR 11
Db 51 RASGPGGGAPR 61

RESULT 9
AAW62584
ID AAW62584 standard; protein; 180 AA.
XX
XX AAW62584;
AC
XX
XX 17-SEP-1998 (first entry)
DT
XX
XX Cancer associated antigen NY-ESO-1.
DE
XX
XX Cancer associated antigen; NY-ESO-1; regression; progression; onset;
KW cancer; treatment; diagnosis.
KW
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH

```

```

FT Misc-difference 7 /note= "potential myristoylation site"
FT FT
FT Misc-difference 9 /note= "potential myristoylation site"
FT FT
FT Misc-difference 11 /note= "potential phosphorylation site"
FT FT
FT Misc-difference 98 /note= "potential phosphorylation site"
FT FT
FT Misc-difference 134 /note= "potential phosphorylation site"
FT FT
FT Misc-difference 138 /note= "potential phosphorylation site"
FT FT
XX WO9814464-A1.
XX
XX 09-APR-1998.
XX
XX 15-SEP-1997; 97WO-US016335.
XX
XX 03-OCT-1996; 96US-00725182.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Chen Y, Scanlan M, Gure A, Old LJ, Jager E, Knuth A;
XX Drijfhout JW;
XX
XX WPI; 1998-286417/25.
XX N-PSDB; AAV38566.
XX
XX New isolated cancer associated antigen - is used to develop products for
XX the diagnosis and treatment of cancers and for monitoring cancer therapy.
XX
XX Claim 8; Fig 3; 49pp; English.
XX
XX The present sequence represents a cancer associated antigen. The clone
XX from which the DNA sequence is obtained is designated NY-ESO-1. The
XX specification described a method for determining regression, progression
XX of onset of a cancerous condition, comprising monitoring a sample from a
XX patient with the cancerous condition for a parameter selected from NY-ESO
XX -1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells
XX specific for the peptide and an MHC molecule with which it non-covalently
XX complexes. Methods for the treatment of a cancerous condition are also
XX described. The NY-ESO-1 protein and peptides derived from it can be used
XX for diagnosis and treatment of cancers and to monitor the efficacy of a
XX therapeutic regime
XX
XX Sequence 180 AA;
SQ
Query Match 100.0%; Score 60; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGGAPR 11
Db 52 RASGPGGGAPR 62

RESULT 10
AAW69665
ID AAW69665 standard; protein; 180 AA.
XX
XX AAW69665;
AC
XX
XX 27-OCT-1998 (first entry)
DT
XX
XX Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
DE
XX
XX Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
KW
XX
XX Homo sapiens.
OS
XX
XX WO9832855-A1.
PN
XX

```


FT Peptide 63. .72 /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 79. .88 /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 79. .87 /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
FT Peptide 82. .91 and HLA-B35"
FT Peptide 82. .90 /note= "Peptide presented by MHC Class I HLA-A1"
FT Peptide 83. .91 /note= "Peptide presented by MHC Class I HLA-A1"
FT Peptide 84. .92 /note= "Peptide presented by MHC Class I HLA-B44"
FT Peptide 87. .96 /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
FT Peptide 88. .96 /note= "Peptide presented by MHC Class I HLA-A1"
FT Peptide 96. .104 /note= "Peptide presented by MHC Class I HLA-B44"
FT Peptide 100. .108 /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 102. .110 /note= "Peptide presented by MHC Class I HLA-B44"
FT Peptide 107. .116 /note= "Peptide presented by MHC Class I HLA-B44"
FT Peptide 110. .118 /note= "Peptide presented by MHC Class I HLA-A24"
FT Peptide 113. .122 /note= "Peptide presented by MHC Class I HLA-B52"
FT Peptide 113. .122 /note= "Peptide presented by MHC Class I HLA-B7 and HLA-
FT Peptide 113. .121 B52"
FT Peptide /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 115. .124 /note= "Peptide presented by MHC Class I HLA-A3"
FT Peptide 118. .126 /note= "Peptide presented by MHC Class I HLA-B35"
FT Peptide 124. .133 /note= "Peptide presented by MHC Class I HLA-B52"
FT Peptide 125. .133 /note= "Peptide presented by MHC Class I HLA-A24"
FT Peptide 138. .147 /note= "Peptide presented by MHC Class I HLA-B8"
FT Peptide 139. .147 /note= "Peptide presented by MHC Class I HLA-B7"
FT Peptide 145. .153 /note= "Peptide presented by MHC Class I HLA-A24 and HLA-
FT Peptide 153. .162 B52"
FT Peptide /note= "Peptide presented by MHC Class I HLA-B52"
FT Peptide 154. .163 /note= "Peptide presented by MHC Class I HLA-B52"
FT Peptide 154. .162 /note= "Peptide presented by MHC Class I HLA-B52"
FT Peptide 156. .167 /note= "Peptide (AAV52434) presented by MHC Class I HLA-
FT Peptide A2"
FT Peptide 158. .166 /note= "Peptide presented by MHC Class I HLA-A3"
FT Peptide 159. .167 /note= "Peptide presented by MHC Class I HLA-A3"
FT Peptide 162. .170 /note= "Peptide presented by MHC Class I HLA-B52"
FT Peptide ‡
FT XX WO9953938-A1.
PN
XX 28-OCT-1999.
PD
XX 24-MAR-1999;
PF 99WO-US006875.
XX
XX 17-APR-1998;
PR 98US-00062422.

PR 02-OCT-1998; 98US-00165546.
XX (LUDW-) LUDWIG INST CANCER RES.
PA
XX Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI Gure A, Ritter G;
XX WPI; 2000-038483/03.
DR N-PSDB; AA238380.
XX
XX Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes.
XX
XX Claim 30; Fig 3; 49pp; English.
XX
XX This sequence represents a human tumour antigen, NY-ESO-1, the cDNA
CC encoding which was isolated from an oesophagus squamous cell cancer CDNA
CC library. Tissue localisation studies revealed it to be expressed at high
CC levels in normal ovary and testis but not in normal colon, kidney, liver,
CC brain, oesophagus and skin. It was expressed in certain tumours and
CC tumour cell lines with some degree of frequency - these included melanoma
CC specimens and cell lines, and breast and bladder cancer specimens, with
CC expression in other tumour types being sporadic. Peptides derived from NY
CC -ESO-1 are bound by both MHC (major histocompatibility complex) Class I
CC and Class II molecules for presentation to T-cells. Peptides AAY52431-
CC Y52434 bind to Class I HLA-A2 molecules, thereby stimulating
CC proliferation of cytotoxic T-cells, while peptides AAY52435-Y52440 bind
CC to Class II HLA-DR53 molecules, stimulating helper T-cell proliferation.
CC The peptides derived from NY-ESO-1 may be used in methods and
CC compositions used for the treatment, diagnosis and prevention of cancers
CC (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma,
CC ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to
CC stimulate the proliferation of T cells
CC
CC Revised record issued on 21-OCT-2004 : Correction to feature table key
CC
XX Sequence 180 AA;
SQ
Query Match 100.0%; Score 60; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASGPGGGAPR 11
|||||||
Db 52 RASGPGGGAPR 62
RESULT 13
AAY70862
ID AAY70862 standard; protein; 180 AA.
XX
AC AAY70862;
XX
DT 31-JUL-2000 (first entry)
XX
DE Human tumour antigen, NY-ESO-1 protein.
XX
KW NY-ESO-1; CAMEL; CTL-recognised Antigen on MELanoma; human; cancer; CTL;
KW cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer;
KW melanoma; immunotherapy; immune response.
OS Homo sapiens.
XX
PN WO200023584-A1.
XX
PD 27-APR-2000.
XX
PF 15-OCT-1999; 99WO-EP007832.
XX
PR 16-OCT-1998; 98EP-00119583.
XX
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (UYHO-) UNIV HOSPITAL LEIDEN.

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XX PI Schrier PI, Aarnoudse CA, Heider K, Klade C;
XX DR WPI; 2000-339685/29.
XX DR N-PSDB; AAD00152.
XX PT Tumor-associated antigen useful for cancer immunotherapy is encoded by
XX FT the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
XX FS Example 3; Page 62-63; 73pp; English.
XX CC The present sequence is the human NY-ESO-1 protein, a tumour antigen,
XX CC identified by screening an esophagus carcinoma cDNA library. This protein
XX CC is derived from open reading frame (ORF)-1 that contain epitopes of
XX CC tumour specific T-cells. NY-ESO-1 is expressed in different tumour types,
XX CC but not in healthy tissues except in testis. It also shows homology with
XX CC the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELanoma)
XX CC protein, a tumour-associated antigen. The tumour-associated antigen
XX CC displayed on melanoma cells is recognised by cytotoxic T lymphocytes.
XX CC This sequence has anticancer activity. CAMEL tumour antigen and
XX CC immunogenic peptides derived from it are useful for cancer immunotherapy.
XX CC They have the potential to induce an immune response, by eliciting a CTL
XX CC response. The DNA molecule is used for the construction of recombinant or
XX CC fusion proteins
XX CC
XX SQ Sequence 180 AA;

Query Match 100.0%; Score 60; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGGAPR 11
DB 52 RASGPGGGAPR 62

RESULT 14
AAB03154
ID AAB03154 standard; protein; 180 AA.
XX AC AAB03154;
XX CT 23-OCT-2000 (first entry)
XX CE Human oesophageal cancer-associated antigen NY-ESO-1.
XX CC Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen;
XX KW oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain;
XX KW antibody; diagnostic marker; drug delivery target.
XX CC
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Modified-site 7
XX FT Modified-site 9 /note= "Potential N-myristoylation site"
XX FT Modified-site 11 /note= "Potential N-myristoylation site"
XX FT Modified-site 98 /note= "Potential O-phosphorylation site"
XX FT Modified-site 134 /note= "Potential O-phosphorylation site"
XX FT Modified-site 138 /note= "Potential O-phosphorylation site"
XX FT Modified-site 152.172 /note= "Potential O-phosphorylation site"
XX FT Domain /note= "Potential transmembrane domain"
XX
XX PN US6069233-A.
XX PD 30-MAY-2000.
XX XX
XX PF 26-JAN-1998; 98US-00013150.

```

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XX 03-OCT-1996; 96US-00725381.
XX (SLOK ) SLOAN KETTERING INST CANCER RES.
XX PA (CORR ) CORNELL RES FOUND INC.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX XX
XX PI Scanlan M, Gure AO, Chen Y, Tureci O, Sahin U, Pfreundschuh M,
XX PI Old LJ;
XX XX
XX DR WPI; 2000-410880/35.
XX DR N-PSDB; AAA61483.
XX PT New isolated esophageal cancer-associated antigen useful as markers for
XX FT producing antibodies and as targets for identifying abnormal conditions,
XX FT e.g. infections and cancer.
XX PS Example 5; Fig 3; 9pp; English.
XX CC This sequence represents a human oesophageal cancer-associated antigen,
XX CC NY-ESO-1. The cDNA encoding this sequence was isolated from a cDNA
XX CC library prepared from a specimen of well-to-moderately differentiated
XX CC squamous cell cancer of the oesophagus. Expression analysis demonstrated
XX CC that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma
XX CC cell lines and in normal ovary and testis tissue, but not in normal
XX CC colon, kidney, liver or brain tissue. Analysis of the amino acid sequence
XX CC of the protein indicates that the protein has a transmembrane domain,
XX CC several N-myristoylation sites and O-phosphorylation sites and that it
XX CC contains antigenic sequences in the N-terminal half of the protein. The
XX CC antigen is useful as an immunogen when combined with an adjuvant, in both
XX CC precursor and post-translationally modified forms, and may be used to
XX CC generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic
XX CC marker for oesophageal cancer, and can be utilised as a marker for the
XX CC targetted delivery of therapeutic agents to oesophageal cancer cells. It
XX CC can also be used to generate diagnostic or therapeutic agents
XX CC
XX SQ Sequence 180 AA;

Query Match 100.0%; Score 60; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGGAPR 11
DB 52 RASGPGGGAPR 62

RESULT 15
AAB69946
ID AAB69946 standard; protein; 180 AA.
XX AC AAB69946;
XX CT 27-APR-2001 (first entry)
XX DE Human NY-ESO-1 protein.
XX XX
XX KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
XX KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
XX KW non-small cell lung carcinoma; tumour status determination.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200107917-A1.
XX PD 01-FEB-2001.
XX XX
XX PF 14-JUL-2000; 2000WO-US019220.
XX XX
XX PR 23-JUL-1999; 99US-00359503.
XX XX
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.

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PA (CORR) CORNELL RES FOUND INC.

XX Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;

XX WPI; 2001-182822/18.

DR N-PSDB; AAF58634.

XX
PT Method useful for determining the status (e.g. progression, regression or
PT stability of the disease) of a cancerous condition, involves determining
PT the levels of NY-ESO-1 specific antibodies in a sample taken from a
PT patient.

XX Example 5; Fig 3; 50pp; English.

XX
CC The present sequence is human NY-ESO-1 protein. It is provided in a
CC specification relating to a method for determining the status of a
CC cancerous condition in a patient with a tumour that expresses NY-ESO-1.
CC The method comprises assaying a sample taken from the patient for
CC antibodies that specifically bind to the NY-ESO-1 and comparing the value
CC obtained to a prior value obtained from assay of a prior sample taken
CC from the patient. Any difference between the values is indicative of a
CC change in status of the cancerous condition. The method is useful for
CC determining whether a cancerous condition is progressing, regressing or
CC remaining stable, in particular in patients receiving treatment for a
CC melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
CC carcinoma

XX SQ Sequence 180 AA;

Query Match 100.0%; Score 60; DB 4; Length 180;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASGPGGGAPR 11

Db 52 RASGPGGGAPR 62

Search completed: March 13, 2006, 19:04:00

Job time : 83.8235 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:04:24 ; Search time 13.0706 Seconds
(without alignments)
80.975 Million cell updates/sec

Title: US-09-529-206E-30
Perfect score: 60
Sequence: 1 RASGPGGAPR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
LisKing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	73.3	3190	2 T13828	CREB-binding prote
2	42	70.0	351	2 S50754	hypothetical prote
3	42	70.0	378	2 C87425	aldose 1-epimerase
4	41	68.3	173	2 AB3648	flagellar basal-bo
5	41	68.3	286	2 S04673	H+-transporting tw
6	41	68.3	357	2 F82878	XAA-PRO aminopepti
7	41	68.3	1207	2 T00378	KIAA0641 protein -
8	40	66.7	335	2 S08341	myristylated alani
9	40	66.7	371	2 T39312	hypothetical prote
10	40	66.7	383	2 A86182	hypothetical prote
11	40	66.7	436	2 T36104	conserved hypothet
12	40	66.7	521	2 A29345	steroid hormone re
13	40	66.7	679	2 S02165	regulatory protein
14	40	66.7	954	2 A87431	regulatory protein
15	39	65.0	103	2 C72683	hypothetical prote
16	39	65.0	114	2 B45036	Pur beta - human (
17	39	65.0	163	2 B87464	competence/damage-
18	39	65.0	166	2 I69006	histocompatibility
19	39	65.0	187	2 T35619	hypothetical prote
20	39	65.0	280	2 F95899	probable transcrip
21	39	65.0	307	2 B72677	hypothetical prote
22	39	65.0	387	2 T52451	endopeptidase Clp
23	39	65.0	466	2 F95307	conserved hypothet
24	39	65.0	474	2 G75580	conserved hypothet
25	39	65.0	566	2 T34842	probable transfera
26	39	65.0	575	2 S35327	protein kinase sgg
27	39	65.0	620	2 T30765	hypothetical prote
28	39	65.0	627	2 T35608	polyketide hydroxy
29	39	65.0	733	2 S10932	probable protein k

30 39 65.0 743 2 C56695 transducin-like en
31 39 65.0 757 2 JC7726 (1->4)-alpha-D-glu
32 39 65.0 886 2 S07132 hypothetical prote
33 39 65.0 1028 2 A56038 DNA-binding protei
34 39 65.0 1067 2 S35423 protein kinase sgg
35 39 65.0 1213 2 S16356 ovo protein - frui
36 39 65.0 1317 2 T03748 apoptosis associat
37 39 65.0 4116 2 T13719 calo protein - fru
38 38 63.3 104 2 C72637 hypothetical prote
39 38 63.3 112 2 C87270 hypothetical prote
40 38 63.3 131 2 C75445 rex-related protei
41 38 63.3 143 2 H87399 peptidyl-trna hydr
42 38 63.3 145 2 AH3506 peptidyl-trna hydr
43 38 63.3 161 2 S12246 anther-specific pr
44 38 63.3 185 2 T36874 hypothetical prote
45 38 63.3 189 2 AE3136 Hypothetical Prote

ALIGNMENTS

RESULT 1

T13828
CREB-binding protein homolog - fruit fly (*Drosophila melanogaster*)
C;Species: *Drosophila melanogaster*
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13828
R;Akimaru, H.; Chen, Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, S.M.; Armstrong, S.; G;
Nature 386, 735-738, 1997
A;Title: *Drosophila* CBP is a co-activator of cubitus interruptus in hedgehog signalling
A;Reference number: Z17785; MUID:97263578; PMID:9109493
A;Accession: T13828
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-3190 <AKI>
A;Cross-references: UNIPROT:O01368; UNIPARC:UPI000003EB83; EMBL:U88570; NID:G1916929; P
C;Genetics:
A;Cross-references: FlyBase:FBgn0015624
A;Map position: X
F;1723-1780/Domain: bromodomain homology <BRO>

Query Match 73.3%; Score 44; DB 2; Length 3190;
Best Local Similarity 77.8%; Pred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SGPGGGAPR 11
:|||||
DB 320 NGPGGGGPR 328

RESULT 2

S50754
hypothetical protein WP6 - *Chlamydomonas eugametos*
C;Species: *Chlamydomonas eugametos*
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S50754
R;Woessner, J.P.; Molendijk, A.J.; van Egmond, P.; Klis, F.M.; Goodenough, U.W.; Haring
Plant Mol. Biol. 26, 947-960, 1994
A;Title: Domain conservation in several volvocalean cell wall proteins.
A;Reference number: S50754; MUID:95093034; PMID:8000007
A;Accession: S50754
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-351 <NOE>
A;Cross-references: UNIPROT:Q39492; UNIPARC:UPI00000A170A; EMBL:L29028; NID:G530877; P

Query Match 70.0%; Score 42; DB 2; Length 351;
Best Local Similarity 80.0%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASGPGGGAP 10
|||||
DB 299 RASPGGGPP 308

```

A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-286 <TYB>
A;Cross-references: UNIPROT:P05436; UNIPARC:UPI0000126582
C;Superfamily: H(+)-transporting ATP synthase gamma chain
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

Query Match      68.3%; Score 41; DB 2; Length 286;
Best Local Similarity 80.0%; Pred. No. 81;
Matches      8; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

QY      2 ASGPGGGAPR 11
      ||| |||||
Db      57 ASGQGAGAPR 66

RESULT 6
F82878
XAA-PRO aminopeptidase U0532 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: F82878
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mi
A;Reference number: A82870
A;Accession: F82878
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <GLA>
A;Cross-references: UNIPARC:UPI000000C1CAC; GB:AE002152; GB:AF222894; NID:g68999532; PIDN:
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: pepp; U0532
A;Genetic code: SGC3
C;Superfamily: X-Pro aminopeptidase

Query Match      68.3%; Score 41; DB 2; Length 357;
Best Local Similarity 77.8%; Pred. No. 97;
Matches      7; Conservative      1; Mismatches      1; Indels      0; Gaps      0;

QY      2 ASGPGGGAP 10
      ||| |||||
Db      193 ASGPNGGSP 201

RESULT 7
T00378
KIAA0641 protein - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Accession: T00378
R;Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N
DNA Res. 5, 169-176, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. X. The complete
A;Reference number: Z14142; MUID:98403880; PMID:9734811
A;Accession: T00378
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1207 <ISH>
A;Cross-references: UNIPARC:UPI0000046CF7; EMBL:AB014541; NID:g3327095; PIDN:BAA31616.1;
C;Genetics:
A;Gene: KIAA0641

Query Match      68.3%; Score 41; DB 2; Length 1207;
Best Local Similarity 70.0%; Pred. No. 2.7e+02;
Matches      7; Conservative      1; Mismatches      2; Indels      0; Gaps      0;

QY      2 ASGPGGGAPR 11
      ||| |||||
Db      757 ATGPGGGQPR 766

Aldose 1-epimerase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: C87425
R;Nierman, W.C.; Feidblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87425
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-378 <STO>
A;Cross-references: UNIPROT:Q9A8D6; UNIPARC:UPI000000C73A0; GB:AE005673; NID:g13422779; E
C;Genetics:
A;Gene: CCI418
C;Superfamily: aldose 1-epimerase

Query Match      70.0%; Score 42; DB 2; Length 378;
Best Local Similarity 77.8%; Pred. No. 74;
Matches      7; Conservative      1; Mismatches      0; Gaps      0;

QY      3 SQPGGGAPR 11
      :|| |||||
Db      282 NGPSSGAPR 290

RESULT 4
AB3648
flagellar basal-body rod protein flgF [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AB3648
R;DelVecchio, V.G.; Kapratl, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
R.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AB3648
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <KSR>
A;Cross-references: UNIPROT:Q8Y4Z4; UNIPARC:UPI0000058740; GB:AE008918; PIDN:AAL54349.1;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI1107
A;Map position: 11

Query Match      68.3%; Score 41; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 53;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      5 PGGGAPR 11
      ||| |||||
Db      132 PGGGAPR 138

RESULT 5
S04673
H+-transporting two-sector ATPase (EC 3.6.3.14) gamma chain - Rhodopsedomonas blastica
C;Species: Rhodopsedomonas blastica
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 31-Dec-2004
C;Accession: S04673
R;Tybulewicz, V.L.J.; Falk, G.; Walker, J.E.
J. Mol. Biol. 179, 185-214, 1984
A;Title: Rhodopsedomonas blastica atp operon. Nucleotide sequence and transcription.
A;Reference number: S04666; MUID:85058188; PMID:6209404
A;Accession: S04673
```

RESULT 8

S08341
 myristoylated alanine-rich protein kinase C substrate - bovine
 N;Alternate names: acidic calmodulin-binding 81K protein (ACAMP-81); MARCKS
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
 C;Accession: S08341; A32904; S29270; A46098; PS0338
 R;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
 Nucleic Acids Res. 17, 3987-3989, 1989
 A;Title: Nucleotide sequence of a cDNA for the bovine myristoylated alanine-rich C kinase
 A;Reference number: S08341; MUID:8928412; PMID:273411
 A;Accession: S08341
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-335 <STU>
 A;Cross-references: UNIPROT:P12624; UNIPARC:UPI000016C340; EMBL:M24638; NID:g163339; PID
 R;Stumpo, D.J.; Graff, J.M.; Albert, K.A.; Greengard, P.; Blackshear, P.J.
 Proc. Natl. Acad. Sci. U.S.A. 86, 4012-4016, 1989
 A;Title: Molecular cloning, characterization, and expression of a cDNA encoding the "80-
 A;Reference number: A32904; MUID:89264553; PMID:2726763
 A;Accession: A32904
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-98, 'Q', 100-335 <ST2>
 A;Cross-references: UNIPARC:UPI000017750A; GB:M24638; GB:M23738
 R;Herget, T.; Brooks, S.P.; Broad, S.; Rozengurt, E.
 Eur. J. Biochem. 209, 7-14, 1992
 A;Title: Relationship between the major protein kinase C substrates acidic 80-kDa protein
 or equivalent genes in different species.
 A;Reference number: S29267; MUID:93011168; PMID:1396720
 A;Accession: S29270
 A;Molecule type: DNA
 A;Residues: 191-253, 'SEE', 257-279, 283-292, 'V', 294, 'PEQE', 299, 'A', 300, 'A', 302-313, 'A', 315
 A;Cross-references: UNIPARC:UPI000017750B
 R;Manenti, S.; Sorokine, O.; Van Dorsselaer, A.; Taniguchi, H.
 J. Biol. Chem. 268, 6878-6881, 1993
 A;Title: Isolation of the non-myristoylated form of a major substrate of protein kinase
 A;Reference number: A46098; MUID:93216617; PMID:8463217
 A;Accession: A46098
 A;Molecule type: protein
 A;Residues: 2-11 <MA>
 A;Cross-references: UNIPARC:UPI000017750C
 R;Mizutani, A.; Tokumitsu, H.; Higaka, H.
 Biochem. Biophys. Res. Commun. 182, 1395-1401, 1992
 A;Title: Acidic calmodulin binding protein, ACAMP-81, is MARCKS protein interacting with
 A;Reference number: PS0338; MUID:92171958; PMID:1540183
 A;Accession: PS0338
 A;Molecule type: protein
 A;Residues: 12-30; 56-69; 88-98, 'AS', 100-103; 104-109, 'E', 111-123; 156-160; 165-171; 196-215; 2
 A;Cross-references: UNIPARC:UPI000017750D; UNIPARC:UPI000017750E; UNIPARC:UPI000017750F;
 514
 A;Experimental source: brain
 A;Note: this sequence is identical with that of myristoylated alanine-rich C-kinase sub
 C;Comment: This protein is a major cellular substrate for protein kinase C and plays a r
 C;Comment: It binds to calmodulin in one to one molar ratio in the presence of calcium a
 C;Genetics:
 A;Introns: 34/3
 C;Keywords: neurofilament triplet H protein
 C;Keywords: actin binding; blocked amino end; calmodulin binding; lipoprotein; myristyla
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F;158,162,166,169/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
 Query Match 66.7%; Score 40; DB 2; Length 335;
 Best Local Similarity 64.3%; Pred. No. 1.3e+02;
 Matches 9; Conservative 1; Mismatches 0; Indels 4; Gaps 1;
 QY 2 ASGPG----GSAPR 11
 Db 288 AAGPGCPAGGAPR 301
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA

RESULT 9

T39312

hypothetical protein SPBC119.14 - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: T39312
 R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
 submitted to the EMBL Data Library, March 1998
 A;Reference number: Z21843
 A;Accession: T39312
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-371 <WOO>
 A;Cross-references: UNIPROT:O42905; UNIPARC:UPI000001352D5; EMBL:AL022117; PIDN:CAAL17929
 A;Experimental source: strain 972h-; cosmid c119
 C;Genetics:
 A;Gene: SPDB:SPBC119.14
 A;Map position: 2
 A;Introns: 77/3; 105/3; 165/3; 250/1; 276/2
 Query Match 66.7%; Score 40; DB 2; Length 371;
 Best Local Similarity 77.8%; Pred. No. 1.4e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RASGPGGGGA 9
 Db 36 RRSFGGGGS 44
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA

RESULT 10
 A86182
 hypothetical protein [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: A86182
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: A86182
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-383 <STO>
 A;Cross-references: UNIPROT:Q9MAT5; UNIPARC:UPI00000A6788; GB:AE005172; NID:g7211979; P
 C;Genetics:
 A;Map position: 1

Query Match 66.7%; Score 40; DB 2; Length 383;
 Best Local Similarity 70.0%; Pred. No. 1.4e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RASGPGGGAP 10
 Db 13 RAAGTGGGGP 22
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA

RESULT 11
 T36104
 conserved hypothetical protein SCE15.01 - Streptomyces coelicolor (fragment)
 C;Species: Streptomyces coelicolor
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: T36104
 R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, April 1999
 A;Reference number: Z21597
 A;Accession: T36104
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA

```

A:Residues: 1-436 <MUR>
A:Cross-references: UNIPROT:Q8CJX1; UNIPARC:UPI000017AD99; EMBL:AL049707; PIDN:CAB41270.
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCE15.01

Query Match      66.7%; Score 40; DB 2; Length 436;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASGPGGGAP 10
Db 153 ASGPGGNTP 161

RESULT 12
A29345      1
steroid hormone receptor ERR1 precursor - human
N:Alternate names: estrogen-related receptor
C:Species: Homo sapiens (nan)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 31-Dec-2004
C:Accession: A29345; A49074
R:Giguere, V.; Yang, N.; Segui, P.; Evans, R.M.
Nature 331, 91-94, 1988
A:Title: Identification of a new class of steroid hormone receptors.
A:Reference number: A29345; MUID:88122546; PMID:3267207
A:Accession: A29345
A:Molecule type: mRNA
A:Residues: 1-521 <GIG>
A:Cross-references: UNIPROT:P11474; UNIPARC:UPI0000142399; EMBL:X51416; NID:g36608; PIDN:
R:Wiley, S.R.; Kraus, R.J.; Zuo, F.; Murray, E.E.; Lortiz, K.; Mertz, J.E.
Genes Dev. 7, 2206-2219, 1993
A:Title: SV40 early-to-late switch involves titration of cellular transcriptional repres
A:Reference number: A49074; MUID:94040741; PMID:8224847
A:Accession: A49074
A:Status: preliminary
A:Molecule type: Protein
A:Residues: 166-169; X', 171-173 <WIL>
A:Cross-references: UNIPARC:UPI000017A1DF
C:Keywords: DNA binding; nucleus; Steroid hormone receptor; transcription regulation; zi
Z:174-434/Domain: erba transforming protein homology <ERBA>
Z:176-196/Region: zinc finger
Z:212-236/Region: zinc finger

Query Match      66.7%; Score 40; DB 2; Length 521;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SGPGGGAPR 11
Db 465 AGPGGAER 473

RESULT 13
S02165      1
regulatory protein flay - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C:Accession: S02165
R:Kaplan, J.B.; Dingwall, A.; Bryan, R.; Champier, R.; Shapiro, L.
J. Mol. Biol. 205, 71-83, 1989
A:Title: Temporal regulation and overlap organization of two Caulobacter flagellar genes
A:Reference number: S02164; MUID:89178645; PMID:2648000
A:Accession: S02165
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-679 <KAP>
A:Cross-references: UNIPROT:P15345; UNIPARC:UPI000017A8F7
C:Genetics:
A:Gene: flay
C:Keywords: transcription regulation

Query Match      66.7%; Score 40; DB 2; Length 679;

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Best Local Similarity 77.8%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASGPGGGAP 10
Db 173 AGPGGAGAP 181

RESULT 14
A87431      1
regulatory protein FlaEY [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: A87431
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: A87431
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-954 <STO>
A:Cross-references: UNIPROT:P15345; UNIPARC:UPI000012A8ED; GB:AE005673; NID:gl3422833; F
C:Genetics:
A:Gene: CCL465

Query Match      66.7%; Score 40; DB 2; Length 954;
Best Local Similarity 77.8%; Pred. No. 3.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASGPGGGAP 10
Db 317 AGPGGAGAP 325

RESULT 15
C72683      1
hypothetical protein APE0884 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: C72683
R:Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: C72683
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-103 <KAW>
A:Cross-references: UNIPROT:Q9YDN0; UNIPARC:UPI000005DD18; DDBJ:AP000060; NID:g5104188;
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0884

Query Match      65.0%; Score 39; DB 2; Length 103;
Best Local Similarity 85.7%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GPGGGAP 10
Db 21 GPGGGSP 27

Search completed: March 13, 2006, 19:16:12
Job time : 14.0706 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 18:53:23 ; Search time 79.8471 Seconds
(without alignments)
97.196 Million cell updates/sec

Title: US-09-529-206E-30
Perfect score: 60
Sequence: 1 RASGPGGGAPR 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 40 summaries

Database :

UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	142	2	Q9NY13_HUMAN
2	60	100.0	180	1	CTG1B_HUMAN
3	60	100.0	180	2	Q7LBY4_HUMAN
4	52	86.7	210	1	CTAG2_HUMAN
5	50	83.3	362	2	Q63Q78_BURPS
6	50	83.3	362	2	Q62H22_BURMA
7	47	78.3	449	2	Q7F1E3_ORYSA
8	47	78.3	895	2	Q4NUK4_9DELT
9	46	76.7	175	1	PACA_CHICK
10	46	76.7	194	2	Q96B02_HUMAN
11	46	76.7	327	2	Q63HT9_BURPS
12	46	76.7	330	2	Q629N3_BURMA
13	46	76.7	383	2	Q4TEG9_TETNG
14	46	76.7	708	2	Q5KJMS_CRYNE
15	46	76.7	708	2	Q55WM1_CRYNE
16	46	76.7	788	2	Q4QP8_HUMAN
17	46	76.7	896	2	Q96D18_HUMAN
18	46	76.7	1000	2	Q4FKF7_9TRYP
19	46	76.7	1253	2	Q6DHV6_HUMAN
20	46	76.7	1430	2	Q9H7P9_HUMAN
21	45	75.0	309	2	Q63N33_BURPS
22	45	75.0	432	2	Q7LOR7_HUMAN
23	45	75.0	444	2	Q9UPQ2_HUMAN
24	45	75.0	504	2	Q4NVJ7_9DELT
25	45	75.0	678	2	Q8NAC4_HUMAN
26	45	75.0	1379	2	Q7QEK5_ANOGA
27	45	75.0	2013	2	Q4NWX4_9DELT
28	44	73.3	159	2	Q4RBL9_TETNG
29	44	73.3	164	2	Q9DW95_RCMVM
30	44	73.3	262	2	Q5ZBE2_ORYSA
31	44	73.3	262	2	Q4NUZ3_9DELT

32	44	73.3	271	2	Q4NAC6_9MICC
33	44	73.3	321	2	Q96S27_HUMAN
34	44	73.3	367	2	Q6AV33_ORYSA
35	44	73.3	398	2	Q8NGH2_HUMAN
36	44	73.3	398	2	Q5SQU1_HUMAN
37	44	73.3	399	2	Q8IVQ3_HUMAN
38	44	73.3	411	2	Q6ERQ1_ORYSA
39	44	73.3	492	2	Q7NWI2_CHRYVO
40	44	73.3	559	2	Q8L680_ORYSA
41	44	73.3	566	2	Q5SQ74_HUMAN
42	44	73.3	580	2	Q7Q0A9_ANOGA
43	44	73.3	584	2	Q5P6Z0_AZOSE
44	44	73.3	702	2	Q4NOM2_9DELT
45	44	73.3	867	2	Q94LD1_ORYSA

ALIGNMENTS

RESULT 1

Q9NY13_HUMAN

ID Q9NY13_HUMAN PRELIMINARY; PRT; 142 AA.

AC Q9NY13;

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)

DE Hypothetical protein LAGE-2 (fragment)

GN Name=LAGE-2;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Lethe B.G.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ275978; CAB76945.1; -; mRNA.

KW Hypothetical protein

FT NON_TER 1

SQ SEQUENCE 142 AA; 13895 MW; 27BBE922ACACCT7B CRC64;

Query Match 100.0%; Score 60; DB 2; Length 142;

Best Local Similarity 100.0%; Pred No. 0.39; Mismatches 0; Indels 0; Gaps 0;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASGPGGGAPR 11

Db 26 RASGPGGGAPR 36

RESULT 2

CTG1B_HUMAN

ID CTG1B_HUMAN STANDARD; PRT; 180 AA.

AC P78358;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-ESO-1).

GN Name=CTAG1B; Synonyms=CTAG, CTAG1;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE-97203161; PubMed-9050879; DOI=10.1073/pnas.94.5.1914;

Chen Y.-T., Scanlan M.J., Sahin U., Tuerci O., Gure A.O., Tsang S.,

Williamson B., Stockert E., Pfrendschuh M., Old L.J.;

"A testicular antigen aberrantly expressed in human cancers detected

by autologous antibody screening."

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EL Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Melanoma;
RX MEDLINE=98289662; PubMed=9626360;
RA Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA de Plaen E., Boon T.;
RT "LAGE-1, a new gene with tumor specificity.";
RL Int. J. Cancer 76:903-908(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98430882; PubMed=9759882;
RA Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,
RA Schwartzentruber D.J., Rosenberg S.A.;
RT "A breast and melanoma-shared tumor antigen: T cell responses to
RT antigenic peptides translated from different open reading frames.";
RL J. Immunol. 161:3596-3606(1998).
CC -!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide
CC variety of cancers. Detected in uterine myometrium.
CC -!- SIMILARITY: Belongs to the CTAG family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U87459; AAB49693.1; -; mRNA.
DR EMBL; AJ003149; CAA05908.1; -; mRNA.
DR EMBL; AF038567; AAD05202.1; -; mRNA.
DR HGNC; HGNC:2491; CTAG1B.
DR MIM; 300156; -.
KW Antigen; Transmembrane.
FT TRANSMEM 156 172 Potential.
FT COMPIAS 5 82 Gly-rich.
SQ SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;

Query Match 100.0%; Score 60; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGGAPR 11
Db 52 RASGPGGGAPR 62

RESULT 3
Q7LBY4 HUMAN
ID Q7LBY4_HUMAN PRELIMINARY; PRT; 180 AA.
AC Q7LBY4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Cancer/testis antigen 1-B (NY-ESO-1/LAGE-2a protein) (Cancer/testis
DE antigen 1-A).
GN Name=CTAG1-B; Synonyms=CTAG1-A, LAGE-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21303268;
RA Galgoczy P., Rosenthal A., Platzer M.;
RT "Human-mouse comparative sequence analysis of the NEMO gene reveals an
RT alternative promoter within the neighboring G6PD gene.";
RL Gene 271:93-98(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21566154; PubMed=11709543; DOI=10.1093/hmg/10.22.2557;
RA Aradhyia S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
RA Patlan H., Ciccodicola A., Kenrick S., Platzer M., D'Urso M.,

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RA Nelson D.L.;
RT "Multiple pathogenic and benign genomic rearrangements occur at a 35
RT kb duplication involving the NEMO and LAGE2 genes.";
RL Hum. Mol. Genet. 10:2557-2567(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Platzer M.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Platzer M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Galgoczy P., Platzer M.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99454989; PubMed=10521621;
RA De Smet C., Lurquin C., Lethe B., Martelange V., Boon T.;
RT "DNA methylation is the primary silencing mechanism for a set of germ
RT line- and tumor-specific genes with a CpG-rich promoter.";
RL Mol. Cell. Biol. 19:7327-7335(1999).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF277315; AAL27014.1; -; Genomic DNA.
DR EMBL; AJ275977; CAB76943.1; -; Genomic DNA.
DR EMBL; AF277315; AAL27013.1; -; Genomic DNA.
SQ SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;

Query Match 100.0%; Score 60; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGGAPR 11
Db 52 RASGPGGGAPR 62

RESULT 4
CTAG2 HUMAN
ID CTAG2_HUMAN STANDARD; PRT; 210 AA.
AC Q75638; Q75637; Q9UB80; Q9UJ89; Q9Y479;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
GN Name=CTAG2; Synonyms=ESO2, LAGE1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B).
RC TISSUE=Melanoma;
RX MEDLINE=98289662; PubMed=9626360;
RA Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
RA de Plaen E., Boon T.;
RT "LAGE-1, a new gene with tumor specificity.";
RL Int. J. Cancer 76:903-908(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORMS LAGE-1A AND LAGE-1B), AND VARIANTS
RP GLN-6; GLN-89 AND ARG-138.
RC TISSUE=Melanoma;
RX MEDLINE=99325550; PubMed=10399963;
RA Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
RT unexpected translation product of LAGE-1.";
RL Int. J. Cancer 82:442-448(1999).
RN [3]

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Qy	1	RASPGGGGAPR 11
Dd	52	RASPGRGGAPR 62
RESULT 5		
Q63QT8_BURPS		
ID	Q63QT8_BURPS PRELIMINARY;	PRT; 362 AA.
AC	Q63QT8;	
DT	25-OCT-2004 (TrEMBLrel. 28, Created)	
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)	
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)	
DE	Putative DNA polymerase III.	
GN	OrderedLocusNames=BFS2936;	
OS	Burkholderia pseudomallei (Pseudomonas pseudomallei).	
OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;	
OC	Burkholderiaceae; Burkholderia; pseudomallei group.	
OX	NCBI_TaxID=28450;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
KC	STRAIN=K96243;	
RX	PubMed=15377794; DOI=10.1073/pnas.0403302101;	
RA	Holden M.T.G., Titchell R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,	
RA	Aikins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,	
RA	Brooks S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,	
RA	Brooke K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,	
RA	Chillingworth T., Cronin A., Crosssett B., Davis P., Deshazer D.,	
RA	Fetwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,	
RA	Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,	
RA	Rabinowitz E., Rutherford K., Sanders M., Simmonds M.,	
RA	Songivailai S., Stevens K., Tumapa S., Vesaratchaveest M.,	
RA	Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;	
RT	"Genomic plasticity of the causative agent of melioidosis,	
RT	Burkholderia pseudomallei.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004) .	
RL	ENML; BX571965; CAH36946.1; -; Genomic DNA.	
DR	GO: GO:0003987; F:DNA-directed DNA polymerase activity; IEA.	
DR	GO: GO:0006260; P:DNA replication; IEA.	
DR	InterPro; IPR010372; DNA pol3 delta.	
DR	InterPro; IPR005790; DNA polIII delta.	
DR	Pfam; PF06144; DNA pol3 delta; 1.	
DR	TIGRFAMs; TIGR01128; hoIA; 1.	
KW	Complete proteome.	
SQ	SEQUENCE 362 AA; 39726 MW; D5FF3DE783D41E41 CRC64;	
Query Match	83.3%; Score 50; DB 2; Length 362;	
Best Local Similarity	81.8%; Pred.No. 28;	
Matches	9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Qy	1	RASPGGGGAPR 11
Dd	349	RAAGPGGDAPR 359
RESULT 6		
Q62H22_BURMA		
ID	Q62H22_BURMA PRELIMINARY;	PRT; 362 AA.
AC	Q62H22;	
DT	25-OCT-2004 (TrEMBLrel. 28, Created)	
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)	
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)	
DE	DNA polymerase III, delta subunit (EC 2.7.7.7).	
GN	Name=hoIA; OrderedLocusNames=BMA2451;	
OS	Burkholderia mallei (Pseudomonas mallei).	
OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;	
OC	Burkholderiaceae; Burkholderia.	
OX	NCBI_TaxID=13373;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
KC	STRAIN=ATCC 23344;	
RX	PubMed=15377793; DOI=10.1073/pnas.0403306101;	
RA	Nierman W.C., DeShazer D., Kim H.S., Tetzelin H., Nelson K.E.,	

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RA  Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA  Daugherty S.C., Davidson T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA  Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA  Madupu R., Mohammud Y., Nelson W.C., Radune D., Romero C.M.,
RA  Sarria S., Sellengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA  Zafar N., Zhou L., Fraser C.M.;
RT  "Structural flexibility in the Burkholderia mallei genome.";
RL  Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251 (2004).
DR  EMBL; CP000010; AAU49707.1; -; Genomic DNA.
DR  TIGR; BNA2451; -.
DR  GO; GO:003887; F:DNA-directed DNA polymerase activity; IEA.
DR  GO; GO:0016740; F:transferase activity; IEA.
DR  GO; GO:006260; P:DNA replication; IEA.
DR  InterPro; IPR010372; DNA_pol3_delta.
DR  InterPro; IPR005790; DNA_pol3_delta.
DR  Pfam; PF06144; DNA_pol3_delta; 1.
DR  TIGRFAMs; TIGR01128; hoiA; 1.
KW  Complete proteome; Nucleotidyltransferase; Transferase.
SQ  SEQUENCE 362 AA; 38726 MW; D5FP3DE783D41E41 CRC64;

Query Match      83.3%; Score 50; DB 2; Length 362;
Best Local Similarity 81.8%; Pred. No. 28;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  1 RASGPGGGAPR 11
DB  349 RAAGPGGDAPR 359
||:|||||

RESULT 7
Q7F1E3_ORYSA PRELIMINARY; PRT; 449 AA.
AC Q7F1E3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein OJ1191_A10.131 (Hypothetical protein
DE OJ1014_E06.5).
GN Name=OJ1191_A10.131; Synonyms=OJ1014_E06.5;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AF003857; BAD08744.1; -; Genomic DNA.
DR EMBL; AP003888; BAD11573.1; -; Genomic DNA.
DR Gramene; Q7F1E3; -.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0045672; F:metal ion binding; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR008700; NOI.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF05627; NOI; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 449 AA; 47196 MW; B8EPF7708B292296 CRC64;

Query Match      78.3%; Score 47; DB 2; Length 449;
Best Local Similarity 81.8%; Pred. No. 94;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1 RASGPGGGAPR 11
DB  349 RAAGPGGDAPR 359
||:|||||

RESULT 9
PACA_CHICK PRELIMINARY; PRT; 175 AA.
AC P41534; Q53WMO;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Glucagon-family neuropeptides precursor [Contains: Growth hormone-
DE releasing factor 1-46 (GRF) (Growth hormone-releasing hormone) (GHRH);
DE Pituitary adenylate cyclase activating polypeptide-27 (PACAP-27)
DE (PACAP27); Pituitary adenylate cyclase activating polypeptide-38
DE (PACAP-38) (PACAP38)].
GN Name=ADCYAP1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].
RX MEDLINE=97174314; PubMed=9022048;
RA McRory J.E., Parker R.L., Sherwood N.M.;
RT "Expression and alternative processing of a chicken gene encoding both
RT growth hormone-releasing hormone and pituitary adenylate cyclase-
RT activating polypeptide.";

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DB  157 RAKGGGGAPR 167
||:|||||

RESULT 8
Q4NUK4_9DELTA PRELIMINARY; PRT; 895 AA.
AC Q4NUK4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE LiGA.
GN ORFNames=AdehdRAFT 2813;
OS Anaeromyxobacter dehalogenans 2CP-C.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cyctobacterineae; Myxococcaceae; Anaeromyxobacter.
OX NCBI_TaxID=290397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Izrani S., Pittluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Anaeromyxobacter
RT dehalogenans 2CP-C.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Anaeromyxobacter
RT dehalogenans 2CP-C.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHD01000013; EAL79351.1; -; Genomic DNA.
SQ SEQUENCE 895 AA; 93871 MW; 0AE25BBBF172BDB0 CRC64;

Query Match      78.3%; Score 47; DB 2; Length 895;
Best Local Similarity 81.8%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1 RASGPGGGAPR 11
DB  799 RARGGGGAPR 809
||:|||||

RESULT 9
PACA_CHICK STANDARD; PRT; 175 AA.
AC P41534; Q53WMO;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Glucagon-family neuropeptides precursor [Contains: Growth hormone-
DE releasing factor 1-46 (GRF) (Growth hormone-releasing hormone) (GHRH);
DE Pituitary adenylate cyclase activating polypeptide-27 (PACAP-27)
DE (PACAP27); Pituitary adenylate cyclase activating polypeptide-38
DE (PACAP-38) (PACAP38)].
GN Name=ADCYAP1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].
RX MEDLINE=97174314; PubMed=9022048;
RA McRory J.E., Parker R.L., Sherwood N.M.;
RT "Expression and alternative processing of a chicken gene encoding both
RT growth hormone-releasing hormone and pituitary adenylate cyclase-
RT activating polypeptide.";

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RL DNA Cell Biol. 16:95-102(1997).
RN [2]
RP PROTEIN SEQUENCE OF 131-168.
RA Yasuhara T., Mizuno K., Somogyvari-Vigh A., Komaki G., Arimura A.;
RT "Isolation and primary structure of chicken PACAP.";
RL Regul. Pept. 37:326-326(1992).
CC -|- FUNCTION: Primary role of GRF is to release GH from the pituitary.
CC -|- FUNCTION: PACAP plays pivotal roles as a neurotransmitter and/or a
CC neuromodulator.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=GRF 1-46;
CC IsoId=P41534-1; Sequence=Displayed;
CC Name=GRF 1-43;
CC IsoId=P41534-2; Sequence=VSP_001760;
CC Name=GRF 33-46;
CC IsoId=P41534-3; Sequence=VSP_001759;
CC -|- SIMILARITY: Belongs to the glucagon family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U71183; AAB51200.1; -; mRNA.
CC EMBL; U71184; AAB51201.1; -; mRNA.
CC EMBL; U71185; AAB51202.1; -; mRNA.
CC EMBL; U67275; AAC64494.1; -; Genomic_DNA.
CC HSSP; P18509; 1GEA.
CC InterPro; IPR000532; Glucagon.
CC Pfam; PF00123; Hormone_2; 2.
CC PRINTS; PR00275; GLUCAGON.
CC PROSITE; PS00260; GLUCAGON; 2.
CC KW Alternative splicing; Amidation; Cleavage on pair of basic residues;
CC Direct protein sequencing; Glucagon family; Hormone; Signal.
CC -----
CC SIGNAL 1 23 Potential.
CC FT PROPEP 24 80 Growth hormone-releasing factor 1-46.
CC FT PEPTIDE 83 128 Pituitary adenylate cyclase activating
CC FT PEPTIDE 131 168 polypeptide-38.
CC FT PEPTIDE 131 157 Pituitary adenylate cyclase activating
CC FT PROPEP 172 175 polypeptide-27.
CC FT MOD_RES 157 157 Leucine amide (G-158 provides amide
CC FT MOD_RES 168 168 group).
CC FT MOD_RES 168 168 Lysine amide (G-169 provides amide
CC FT VARSPLIC 82 114 group).
CC FT VARSPLIC 82 114 RHADGIFSKAYRKLGLQLSARNYLHSLMAKRVG -> S
CC FT VARSPLIC 115 117 (in isoform GRF 33-46).
CC FT VARSPLIC 117 117 /FTId=VSP_001759.
CC FT VARSPLIC 117 117 Missing (in isoform GRF 1-43).
CC FT VARSPLIC 117 117 /FTId=VSP_001760.
CC SQ SEQUENCE 175 AA; 19561 MW; 0DB54955F0AA9DFB CRC64;
Query Match 76.7%; Score 46; DB 1; Length 175;
Best Local Similarity 72.7%; Pred. No. 52;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 RASGPGGGAPR 11
DB 56 RAGAPGGGGPR 66
RESULT 10
Q96B02 HUMAN
ID Q96B02_HUMAN PRELIMINARY; PRT; 194 AA.
AC Q96B02;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PLEKHG2 protein (Fragment).

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GN Name=PLEKHG2;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywicki M.I., Skaleka U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pituitary;
RA Director MGC Project;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015174; AAH15174.1; -; mRNA.
FT NON_TER 1
SQ SEQUENCE 194 AA; 19957 MW; 91AB4FF8F05C8D3C CRC64;
Query Match 76.7%; Score 46; DB 2; Length 194;
Best Local Similarity 80.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 RASGPGGGAP 10
DB 100 RQGPGGGGAP 109
RESULT 11
Q63HT9 BURPS
ID Q63HT9_BURPS PRELIMINARY; PRT; 327 AA.
AC Q63HT9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative lipoprotein.
GN OrderedLocusNames=BFSS2331;
OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; pseudomallei group.
OX NCBI_TaxID=28450;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K96243;
RX PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdano-Tarraga A.-M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosset B., Davis P., Deshazer D.,
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitz E., Rutherford K., Sanders M., Simmonds M.,

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RA Songvilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR EMBL; BX571966; CAH39817.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR007428; VAcJ.
DR Pfam; PF04333; VAcJ; 1.
DR PRINTS; PRO1805; VACJLIPROT.
KW Complete proteome; Lipoprotein.
SQ SEQUENCE 327 AA; 33687 MW; AC5D2C7CC4A4A25 CRC64;

Query Match 76.7%; Score 46; DB 2; Length 327;
Best Local Similarity 88.9%; Pred. No. 96;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 2 ASGPGGGAP 10
Db 243 AGPGGGAP 251

RESULT 12
Q629N3_BURMA PRELIMINARY; PRT; 330 AA.
AC Q629N3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Putative lipoprotein.
GN OrderedLocusNames=BMAA2092;
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=13373;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 23344;
RX PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA Daugherty S.C., Davidgen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA Madupu S., Mohammed Y., Nelson W.C., Radu D., Romero C.M.,
RA Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA Zafar N., Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR EMBL; CP000011; AAU47030.1; -; Genomic_DNA.
DR TIGR; BMAA2092; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR007428; VAcJ.
DR Pfam; PF04333; VAcJ; 1.
DR PRINTS; PRO1805; VACJLIPROT.
XW Complete proteome; Lipoprotein.
SQ SEQUENCE 330 AA; 33977 MW; 2F12165CD7366835 CRC64;

Query Match 76.7%; Score 46; DB 2; Length 330;
Best Local Similarity 88.9%; Pred. No. 97;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 2 ASGPGGGAP 10
Db 243 AGPGGGAP 251

RESULT 13
Q4TEG9_TETNG PRELIMINARY; PRT; 383 AA.
AC Q4TEG9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

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DE Chromosome undetermined SCAF5395, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00002257001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Bieumont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01005395; CAF88713.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 383 AA; 39582 MW; A61F4ECF2EEC3861 CRC64;

Query Match 76.7%; Score 46; DB 2; Length 383;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 1 RASGPGGGAP 10
Db 168 RQPGGGAP 177

RESULT 14
Q5KJMS_CRYNE PRELIMINARY; PRT; 708 AA.
AC Q5KJMS;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Actin cross-linking, putative.
GN ORFNames=CNC06000;
OS Cryptococcus neoformans var. neoformans JEC21.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=214684;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JEC21;
RA Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Uterback T.,
RA Van Aken S., Fraser C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=JEC21;
RX PubMed=15853466; DOI=10.1126/science.1103773;
RA Loftus B., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,

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RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
RA Kwon-Chung K.J., Lengeller K.B., Maiti R., Marra M.A., Marra R.E.,
RA Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L.,
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA Suh B.B., Tenney A., Uterback T.R., Wickes B.L., Wortman J.R.,
RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
RA Fraser C.M., Hyman R.W.;
RT "The genome of the basidiomycetous yeast and human pathogen
RT Cryptococcus neoformans.";
RL Science 307:1321-1324(2005).
DR EMBL; AE017343; AAM42672.1; -; Genomic_DNA.
DR GO; GO:0003779; F:actin binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR001589; Actinin actin bd.
DR InterPro; IPR001715; Calponin act_bd.
DR InterPro; IPR011992; EF-Hand_Type.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF00307; CH; 2.
DR SMART; SM00033; CH; 2.
DR PROSITE; PS00019; ACTININ_1; UNKNOWN_1.
DR PROSITE; PS00020; ACTININ_2; 1.
DR PROSITE; PS50021; CH; 2.
KW Complete proteome.
SQ SEQUENCE 708 AA; 79873 MW; BAF52D1DD2C99B9D CRC64;

Query Match 76.7%; Score 46; DB 2; Length 708;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASGPGGGAP 10
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Db 47 AGGPGGGAP 55

RESULT 15
ID Q55WM1_CRYNE PRELIMINARY; PRT; 708 AA.
AC Q55WM1;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=CNBC1180;
OS Cryptococcus neoformans var. neoformans B-3501A.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=283643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B-3501A;
RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
RA Wickes B.L., Fu J., Davis R.W.;
RT "Cryptococcus neoformans serotype D sequencing.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AEY0100013; EAL21978.1; -; Genomic_DNA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR001589; Actinin actin bd.
DR InterPro; IPR001715; Calponin act_bd.
DR InterPro; IPR011992; EF-Hand_Type.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF00307; CH; 2.
DR SMART; SM00033; CH; 2.
DR PROSITE; PS00019; ACTININ_1; UNKNOWN_1.
DR PROSITE; PS00020; ACTININ_2; UNKNOWN_1.
DR PROSITE; PS50021; CH; 2.
KW Hypothetical protein.
SQ SEQUENCE 708 AA; 79873 MW; BAF52D1DD2C99B9D CRC64;

Query Match 76.7%; Score 46; DB 2; Length 708;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 ASGPGGGAP 10
| | | | |
Db 47 AGGPGGGAP 55

Search completed: March 13, 2006, 19:14:29
Job time : 80.8471 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:14:49 ; Search time 20.4471 Seconds
(without alignments)
44.477 Million cell updates/sec

Title: US-09-529-206E-30
Perfect score: 60
Sequence: 1 RASGPGGAPR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/ptodata/1/iaa/H COMB.pdp.*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pdp.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pdp.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	180	1	US-08-791-495-9
2	60	100.0	180	2	US-08-937-263B-8
3	60	100.0	180	2	US-09-751-798-8
4	60	100.0	180	2	US-09-392-714-25
5	60	100.0	180	2	US-09-165-546D-15
6	60	100.0	180	2	US-09-341-829A-9
7	60	100.0	180	2	US-09-849-602-30
8	52	86.7	180	1	US-08-791-495-7
9	52	86.7	180	2	US-09-341-829A-7
10	52	86.7	210	1	US-08-791-495-5
11	52	86.7	210	2	US-09-341-829A-5
12	48	80.0	9	2	US-09-344-040C-117
13	48	80.0	9	2	US-09-833-039A-117
14	48	80.0	809	2	US-09-252-991A-31759
15	46	76.7	143	2	US-08-789-329C-10
16	46	76.7	160	2	US-09-252-991A-17249
17	46	76.7	172	2	US-08-789-329C-7
18	46	76.7	175	2	US-08-789-329C-3
19	45	75.0	421	2	US-09-252-991A-32326
20	45	75.0	678	2	US-10-104-047-3295
21	45	75.0	1427	2	US-09-252-991A-20577
22	44	73.3	196	2	US-09-252-991A-30527
23	44	73.3	456	2	US-09-252-991A-17335
24	43	71.7	210	2	US-09-252-991A-24923
25	43	71.7	1228	2	US-09-252-991A-17764
26	42	70.0	283	2	US-09-252-991A-17831
27	42	70.0	836	2	US-09-491-356C-21

28	41	68.3	177	2	US-09-252-991A-18782	Sequence 18782, A
29	41	68.3	310	2	US-09-252-991A-19986	Sequence 19986, A
30	41	68.3	340	2	US-09-949-002-562	Sequence 562, App
31	41	68.3	412	1	US-08-878-989-6	Sequence 6, Appli
32	41	68.3	412	2	US-09-272-796-6	Sequence 6, Appli
33	41	68.3	416	2	US-09-252-991A-30219	Sequence 30219, A
34	41	68.3	536	2	US-10-104-047-3369	Sequence 3369, Ap
35	41	68.3	555	2	US-09-252-991A-17549	Sequence 17549, A
36	41	68.3	563	2	US-09-252-991A-27111	Sequence 27111, A
37	41	68.3	679	2	US-09-252-991A-32992	Sequence 32992, A
38	41	68.3	807	2	US-09-252-991A-31361	Sequence 31361, A
39	41	68.3	1000	2	US-10-098-600B-16	Sequence 16, Appl
40	41	68.3	1207	2	US-09-949-002-376	Sequence 376, App
41	41	68.3	1323	2	US-09-248-796A-19543	Sequence 19543, A
42	41	68.3	1384	2	US-08-976-255-11	Sequence 11, Appl
43	41	66.7	137	2	US-09-252-991A-20489	Sequence 20489, A
44	40	66.7	174	2	US-09-902-540-12423	Sequence 12423, A
45	40	66.7				

ALIGNMENTS

RESULT 1
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 60; DB 1; Length 180;

Best Local Similarity 100.0%; Pred No. 0.69;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGAPR 11

DB 52 RASGPGGAPR 62

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RESULT 2
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-937-263B-8
Query Match 100.0%; Score 60; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGGAPR 11
Db 52 RASGPGGGAPR 62

RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
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; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6525177man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
;
US-09-751-798-8
Query Match 100.0%; Score 60; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGGAPR 11
Db 52 RASGPGGGAPR 62

RESULT 4
US-09-392-714-25
; Sequence 25, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-392-714-25
Query Match 100.0%; Score 60; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGGAPR 11
Db 52 RASGPGGGAPR 62
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RESULT 5
US-09-165-546D-15
; Sequence 15, Application US/09165546D
; Patent No. 6723832
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
;           Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
;                   SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
;                   USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546D
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6723832man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15
;
Query Match 100.0%; Score 60; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGGAPR 11
Db 52 RASGPGGGAPR 62

RESULT 6
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
;
Query Match 100.0%; Score 60; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGGAPR 11
Db 52 RASGPGGGAPR 62

RESULT 7
US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30
;
Query Match 100.0%; Score 60; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGGAPR 11
Db 52 RASGPGGGAPR 62

RESULT 8
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-9
;
Query Match 100.0%; Score 60; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGGAPR 11
Db 52 RASGPGGGAPR 62

RESULT 7
US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30
;
Query Match 100.0%; Score 60; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGGAPR 11
Db 52 RASGPGGGAPR 62

RESULT 8
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-7

Query Match      86.7%; Score 52; DB 1; Length 180;
Best Local Similarity 90.9%; Pred. No. 7.5;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 RASGPGGGAPR 11
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Db      52 RASGPRGGAPR 62

RESULT 9
US-09-341-829A-7
; Sequence 7, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-7

Query Match      86.7%; Score 52; DB 2; Length 180;
Best Local Similarity 90.9%; Pred. No. 7.5;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 RASGPGGGAPR 11
      ||||| |||||
Db      52 RASGPRGGAPR 62

RESULT 10
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

```

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; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-5

Query Match      86.7%; Score 52; DB 1; Length 210;
Best Local Similarity 90.9%; Pred. No. 8.6;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 RASGPGGGAPR 11
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Db      52 RASGPRGGAPR 62

RESULT 11
US-09-341-829A-5
; Sequence 5, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-5

Query Match      86.7%; Score 52; DB 2; Length 210;
Best Local Similarity 90.9%; Pred. No. 8.6;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      1 RASGPGGGAPR 11
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Db      52 RASGPRGGAPR 62

RESULT 12

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US-09-344-040C-117
; Sequence 117, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determining
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 117
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-117

Query Match 80.0%; Score 48; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGGA 9
|||
DB 1 RASGPGGGA 9

RESULT 13
US-09-833-039A-117
; Sequence 117, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 117
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-117

Query Match 80.0%; Score 48; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGGA 9
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DB 1 RASGPGGGA 9

RESULT 14
US-09-252-991A-31759
; Sequence 31759, Application US/09252991A

; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31759
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31759

Query Match 80.0%; Score 48; DB 2; Length 809;
Best Local Similarity 81.8%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RASGPGGAPR 11
|||
DB 244 RAGGPRGGAPR 254

RESULT 15
US-08-789-329C-10
; Sequence 10, Application US/08789329C
; Patent No. 6165755
; GENERAL INFORMATION:
; APPLICANT: SHERWOOD ET AL.
; TITLE OF INVENTION: CHICKEN NEUROPEPTIDE GENE USEFUL
; TITLE OF INVENTION: FOR IMPROVED POULTRY PRODUCTION
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204-2988
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: WordPerfect 7.0 & ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,329C
; FILING DATE: 01/23/97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Barp, David J.
; REGISTRATION NUMBER: 41,401
; REFERENCE/DOCKET NUMBER: 2847-46468/DJE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 143 aa
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-789-329C-10

Query Match 76.7%; Score 46; DB 2; Length 143;
Best Local Similarity 72.7%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RASGPGGGAPR 11
||| ||| |||
Db 56 RAGAPGGGGPR 66

Search completed: March 13, 2006, 19:18:52
Job time : 20.4471 secs

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r

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 13, 2006, 19:51:56 ; Search time 66.5176 Seconds
(without alignments)
69.096 Million cell updates/sec

Title: US-09-529-206E-30
Perfect score: 60
Sequence: 1 RASGPGGAPR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	30	4	US-10-296-734-1404
2	60	100.0	179	5	US-10-482-029-202
3	60	100.0	180	3	US-09-751-798-8
4	60	100.0	180	3	US-09-849-602-30
5	60	100.0	180	4	US-10-023-182-8
6	60	100.0	180	4	US-10-207-655-71
7	60	100.0	180	4	US-10-364-614-14
8	60	100.0	180	4	US-10-026-066-3
9	60	100.0	180	4	US-10-117-937-74
10	60	100.0	180	4	US-10-295-027-386
11	60	100.0	180	4	US-10-296-734-832
12	60	100.0	180	4	US-10-188-832-139
13	60	100.0	180	4	US-10-777-053-11
14	60	100.0	180	4	US-10-751-088-15
15	60	100.0	180	4	US-10-657-022-74
16	60	100.0	180	4	US-10-837-217-11
17	60	100.0	180	5	US-10-877-373-9
18	60	100.0	180	5	US-10-723-860-1270
19	60	100.0	180	5	US-10-871-708-7
20	60	100.0	180	5	US-10-895-523-3
21	60	100.0	180	5	US-10-182-506A-3
22	60	100.0	180	5	US-10-756-149-5024
23	60	100.0	180	6	US-11-067-064-74
24	60	100.0	180	6	US-11-067-159-74
25	60	100.0	397	3	US-09-821-883-27
26	60	100.0	397	6	US-11-144-912-27
27	60	100.0	3541	4	US-10-296-734-1454

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28 55 91.7 10 4 US-10-447-161-39 Sequence 39, Appl
29 55 91.7 10 4 US-10-415-841A-52 Sequence 52, Appl
30 55 91.7 10 5 US-10-182-506A-23 Sequence 23, Appl
31 52 86.7 30 4 US-10-296-734-1436 Sequence 1436, Ap
32 52 86.7 135 4 US-10-295-027-388 Sequence 388, App
33 52 86.7 135 4 US-10-188-832-141 Sequence 141, App
34 52 86.7 180 4 US-10-146-473-69 Sequence 69, Appl
35 52 86.7 180 4 US-10-117-937-75 Sequence 75, Appl
36 52 86.7 180 4 US-10-296-734-834 Sequence 834, App
37 52 86.7 180 4 US-10-468-406-4 Sequence 4, Appl
38 52 86.7 180 4 US-10-657-022-75 Sequence 75, Appl
39 52 86.7 180 5 US-10-877-373-7 Sequence 7, Appl
40 52 86.7 180 6 US-11-067-064-75 Sequence 75, Appl
41 52 86.7 180 6 US-11-067-159-75 Sequence 75, Appl
42 52 86.7 210 4 US-10-157-031-88 Sequence 88, Appl
43 52 86.7 210 4 US-10-117-937-76 Sequence 76, Appl
44 52 86.7 210 4 US-10-657-022-76 Sequence 76, Appl
45 52 86.7 210 5 US-10-877-373-5 Sequence 5, Appl

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ALIGNMENTS

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RESULT 1
US-10-296-734-1404
; Sequence 1404, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1404
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA segment 4
US-10-296-734-1404

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Query Match 100.0%; Score 60; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 RASGPGGAPR 11
Db 9 RASGPGGAPR 19

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RESULT 2
US-10-482-029-202
; Sequence 202, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-202

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Query Match      100.0%; Score 60; DB 5; Length 179;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASGPGGGAPR 11
Db      52 RASGPGGGAPR 62

RESULT 3
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. US20020010321A1
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. US20020010321A1man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-09-751-798-8

Query Match      100.0%; Score 60; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASGPGGGAPR 11
Db      52 RASGPGGGAPR 62

RESULT 4
US-09-849-602-30
; Sequence 30, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
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Query Match      100.0%; Score 60; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASGPGGGAPR 11
Db 52 RASGPGGGAPR 62

RESULT 6
US-10-207-655-71
; Sequence 71, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-71

Query Match      100.0%; Score 60; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASGPGGGAPR 11
Db 52 RASGPGGGAPR 62

RESULT 7
US-10-364-614-14
; Sequence 14, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
; APPLICANT: JAGER, Elke
; APPLICANT: KNUTH, Alexander
; APPLICANT: OLD, Lloyd
; APPLICANT: Grjatic, Sacha
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
; FILE REFERENCE: LUD 5726.1 CIP
; CURRENT APPLICATION NUMBER: US/10/364,614
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/355,828
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-614-14

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Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASGPGGGAPR 11
Db 52 RASGPGGGAPR 62

RESULT 8
US-10-026-066-3
; Sequence 3, Application US/10026066
; Publication No. US20030215425A1
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; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
; TITLE OF INVENTION: PRESENTING CELLS
; FILE REFERENCE: CTLM.21CPI
; CURRENT APPLICATION NUMBER: US/10/026,066
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-026-066-3

Query Match      100.0%; Score 60; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASGPGGGAPR 11
Db 52 RASGPGGGAPR 62

RESULT 9
US-10-117-937-74
; Sequence 74, Application US/10117937
; Publication No. US2003020239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-74

Query Match      100.0%; Score 60; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASGPGGGAPR 11
Db 52 RASGPGGGAPR 62

RESULT 10
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US-10-295-027-386
; Sequence 386, Application US/10295027
; Publication No. US2003023250A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-03-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 386
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-386

Query Match          100.0%; Score 60; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASGPGGGAPR 11
Db      52 RASGPGGGAPR 62

RESULT 11
US-10-296-734-832
; Sequence 832, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR APPLICATION NUMBER: 2003-08-04
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 832
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US-10-295-027-386
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYNSOLA consensus polypeptide
US-10-296-734-832

Query Match          100.0%; Score 60; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASGPGGGAPR 11
Db      52 RASGPGGGAPR 62

RESULT 12
US-10-188-832-139
; Sequence 139, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-139

Query Match          100.0%; Score 60; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASGPGGGAPR 11
Db      52 RASGPGGGAPR 62

RESULT 13
US-10-777-053-11
; Sequence 11, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: MANNK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
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; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-777-053-11

Query Match 100.0%; Score 60; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGGAPR 11
Db 52 RASGPGGGAPR 62

RESULT 14

US-10-751-088-15
; Sequence 15, Application US/10751088
; Publication No. US2004015804A1
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
; USES THEREOF

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: FULBRIGHT & JAWORSKI LLP

STREET: 666 Fifth Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10158

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/751,088

FILING DATE: 02-Jan-2004

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/165,546D

FILING DATE: 02-Oct-1998

APPLICATION NUMBER: 09/062,422

FILING DATE: April 17, 1998

APPLICATION NUMBER: 08/937,263

FILING DATE: September 15, 1997

APPLICATION NUMBER: US 08/725,182

FILING DATE: October 3, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, Norman D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 318-3000

TELEFAX: (212) 318-3400

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 180 amino acids

TYPE: amino acid

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 15

US-10-751-088-15

Query Match 100.0%; Score 60; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGGAPR 11
Db 52 RASGPGGGAPR 62

RESULT 15

US-10-657-022-74
; Sequence 74, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANNK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-657-022-74

Query Match 100.0%; Score 60; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASGPGGGAPR 11
Db 52 RASGPGGGAPR 62

Search completed: March 13, 2006, 20:02:27
Job time : 66.5176 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 13, 2006, 19:54:06 ; Search time 7.50588 Seconds
(without alignments)
40.793 Million cell updates/sec

Title: US-09-529-206E-30
Perfect score: 60
Sequence: 1 RASGPGGAPR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 161667 seqs, 27834885 residues

Total number of hits, satisfying chosen parameters: 161667

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.New.*
1: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pap.*
2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pap.*
3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pap.*
4: /cgn2_6/prodata/1/pubpaa/PCR_NEW_PUB.pap.*
5: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pap.*
6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pap.*
7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pap.*
8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	60	100.0	180	7	US-11-155-288-7
2	60	100.0	240	7	US-11-021-441-28
3	48	80.0	20	6	US-10-623-155-496
4	45	75.0	678	7	US-11-072-512-3295
5	43	71.7	306	7	US-11-096-568A-20556
6	42	70.0	134	7	US-11-096-568A-23806
7	41	68.3	365	7	US-11-108-528-58
8	41	68.3	537	7	US-11-179-958A-2
9	41	68.3	555	7	US-11-072-512-3369
10	41	68.3	953	7	US-11-037-243-66
11	40.5	67.5	280	7	US-11-143-980-34
12	40	66.7	558	7	US-11-096-568A-26217
13	40	66.7	974	6	US-10-531-036-35
14	40	66.7	1832	7	US-11-087-099-7762
15	39	65.0	213	7	US-11-072-512-2722
16	39	65.0	233	7	US-11-240-769-58
17	39	65.0	353	7	US-11-096-568A-22334
18	39	65.0	358	7	US-11-096-568A-22333
19	39	65.0	413	7	US-11-096-568A-27265
20	39	65.0	420	7	US-11-096-568A-22332
21	39	65.0	430	6	US-10-992-577-8
22	39	65.0	430	6	US-10-508-892-2
23	39	65.0	430	7	US-11-223-294-54
24	39	65.0	618	7	US-11-078-735-18
25	39	65.0	618	7	US-11-050-346-63

26	39	65.0	618	7	US-11-103-077-18	Sequence 18, Appl
27	39	65.0	662	7	US-11-072-175-184	Sequence 184, App
28	38	63.3	132	7	US-11-096-568A-14323	Sequence 14323, A
29	38	63.3	228	7	US-11-096-568A-16457	Sequence 16457, A
30	38	63.3	236	7	US-11-096-568A-22845	Sequence 22845, A
31	38	63.3	274	7	US-11-096-568A-22603	Sequence 22603, A
32	38	63.3	306	7	US-11-096-568A-12071	Sequence 12071, A
33	38	63.3	320	7	US-11-096-568A-988	Sequence 988, App
34	38	63.3	438	6	US-10-650-328B-9	Sequence 9, Appli
35	38	63.3	459	7	US-11-096-568A-21887	Sequence 21887, A
36	38	63.3	1121	7	US-11-087-099-9800	Sequence 9800, Ap
37	38	63.3	1121	7	US-11-087-099-11165	Sequence 11165, A
38	37	61.7	152	7	US-11-096-568A-342	Sequence 342, App
39	37	61.7	167	7	US-11-096-568A-10542	Sequence 10542, A
40	37	61.7	189	7	US-11-107-029-4	Sequence 4, Appli
41	37	61.7	198	7	US-11-096-568A-22494	Sequence 22494, A
42	37	61.7	269	7	US-11-096-568A-22493	Sequence 22493, A
43	37	61.7	328	7	US-11-096-568A-11283	Sequence 11283, A
44	37	61.7	375	7	US-11-096-568A-24377	Sequence 24377, A
45	37	61.7	379	7	US-11-109-156-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-11-155-288-7
; Sequence 7, Application US/11155288
; Publication No. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J. L.
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.050A
; CURRENT FILING DATE: 2005-06-17
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-7

Query Match 100.0%; Score 60; DB 7; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.092; 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0;
QY 1 RASGPGGAPR 11
DB 52 RASGPGGAPR 62

RESULT 2
US-11-021-441-28
; Sequence 28, Application US/11021441
; Publication No. US20050249748A1
; GENERAL INFORMATION:
; APPLICANT: DUBENSKY, Thomas W., Jr.
; APPLICANT: PORTNOY, Daniel A.
; APPLICANT: LUCKETT, William S., Jr.
; APPLICANT: COOK, David N.
; TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
; TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
; TITLE OF INVENTION: THEROP
; FILE REFERENCE: 282172003900
; CURRENT APPLICATION NUMBER: US/11/021,441
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: US 60/616,750
; PRIOR FILING DATE: 2004-10-06

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; PRIOR APPLICATION NUMBER: US 60/515,287
; PRIOR FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/599,377
; PRIOR FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: PCT/US2004/2388
; PRIOR FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US 10/883,599
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/556,744
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; 1 OTHER INFORMATION: Fusion protein
US-11-021-441-28

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Query Match	100.0%	Score 60;	DB 7;	Length 240;
Best Local Similarity	100.0%;	Pred. No. 0.12;		
Matches 11; Conservative 0;	Mismatches 0;	Indels		
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Db	112	RASGPGGGCAPR	122	

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RESULT 3
JS-10-623-155-496
; Sequence 496, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Rettet, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 496
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-496

```

Query Match	80.0%	Score 48	DB 6	Length 20
Best Local Similarity	100.0%	Pred. No. 0.6		
Matches	9	Conservative	0	Mismatches
			0	Indels
			0	Gaps

RESULT 4
US-11-072-512-3295
; Sequence 3295, Application US/11072512
; Publication No. US2006029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO

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/ APPLICANT: HIO, YURI
/ APPLICANT: OTSUKA, KAORU
/ APPLICANT: NAGAI, KEIICHI
/ APPLICANT: IRIE, RYOTARO
/ APPLICANT: TAMECHIKA, ICHIRO
/ APPLICANT: SEKI, NAOHICO
/ APPLICANT: YOSHIKAWA, TSUTOMU
/ APPLICANT: OTSUKA, MOTOUYUKI
/ APPLICANT: NAGAHARI, KENJI
/ APPLICANT: MASUHO, YASUHIKO
/ TITLE OF INVENTION: Novel full length cDNA
/ FILE REFERENCE: 084335-0191
/ CURRENT APPLICATION NUMBER: US/11/072,512
/ PRIOR FILING DATE: 2005-03-07
/ PRIOR APPLICATION NUMBER: US 60/350,978
/ PRIOR FILING DATE: 2002-01-25
/ PRIOR APPLICATION NUMBER: JP 2001-379298
/ PRIOR FILING DATE: 2001-11-05
/ NUMBER OF SEQ ID NOS: 4096
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3295
/ LENGTH: 678
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-11-072-512-3295

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Query Match      75.0%; Score 45; DB 7; Length 678;
Best Local Similarity 80.0%; Pred. No. 30;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASGPGGGAP 10
Db      592 RAAGPGGGWP 601

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RESULT 5
US-11-096-568A-20556
; Sequence 20556, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20556
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(306)
; OTHER INFORMATION: Ceres Seq. ID no. 12383286
US-11-096-568A-20556

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Query Match	71.7%	Score 43;	DB 7;	Length 306;
Best Local Similarity	80.0%	Pred. No. 29;		
Matches	8;	Conservative	0;	Mismatches 2; Indels 0; Gaps 0;
Qy	1	RASGPGGGAP	10	
Db	92	RADGPGTGAP	101	

RESULT 6

US-11-096-568A-23806

; Sequence 23806, Application US/11096568A

; Publication No. US20060048240A1

; GENERAL INFORMATION:

; APPLICANT: Alexandrov, Nikolai et al.

; TITLE OF INVENTION: Sequence-determined

; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23806
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(134)
; OTHER INFORMATION: Ceres Seq. ID no. 12415289
US-11-096-568A-23806

Query Match 70.0%; Score 42; DB 7; Length 134;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RASGPGGGAP 10
| : ||| |||
Db 70 RGAGPGGAGP 79

RESULT 7
US-11-108-528-58
; Sequence 58, Application US/11108528
; Publication No. US20050261189A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Glenn
; APPLICANT: Marvin, Martha
; APPLICANT: Li, Dean Y.
; APPLICANT: Wang, Elizabeth
; APPLICANT: Chen, C. M. Amy
; APPLICANT: Shamah, Steven M.
; TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
; FILE REFERENCE: HYDR-P01-041
; CURRENT APPLICATION NUMBER: US/11/108,528
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,137
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/598,368
; PRIOR FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Mouse
US-11-108-528-58

Query Match 68.3%; Score 41; DB 7; Length 365;
Best Local Similarity 80.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 RASGPGGGAP 10
| : ||| |||
Db 273 RASGPGGGDP 282

RESULT 8
US-11-179-958A-2
; Sequence 2, Application US/11179958A
; Publication No. US20060030537A1
; GENERAL INFORMATION:
; APPLICANT: Chalfant, Charles E.
; APPLICANT: Hannun, Yusef A.
; APPLICANT: Pettus, Benjamin J.
; APPLICANT: Bielawska, Alicja
; TITLE OF INVENTION: Ceramide Kinase and Uses Thereof
; FILE REFERENCE: 9175-028-999 (MUSC Ref P0401)
; CURRENT APPLICATION NUMBER: US/11/179,958A

; CURRENT FILING DATE: 2005-07-11
; PRIOR APPLICATION NUMBER: 60/586,909
; PRIOR FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human ceramide kinase
US-11-179-958A-2

Query Match 68.3%; Score 41; DB 7; Length 537;
Best Local Similarity 70.0%; Pred. No. 86;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RASGPGGGAP 10
| : ||| |||
Db 36 RSPGPGGAGP 45

RESULT 9
US-11-072-512-3369
; Sequence 3369, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3369
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3369

Query Match 68.3%; Score 41; DB 7; Length 555;
Best Local Similarity 77.8%; Pred. No. 88;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 ASGPGGGAP 10
| : ||| |||
Db 473 ASGPGGGSP 481
RESULT 10
US-11-037-243-66
; Sequence 66, Application US/11037243

; Publication No. US20050287546A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEL, SEAN
; APPLICANT: CHARVETZAK, GLEN
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/11/037,243
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: US/09/888,615
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 953
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-037-243-66

Query Match 68.3%; Score 41; DB 7; Length 953;
Best Local Similarity 87.5%; Pred. No. 1.4e+02; Length 953;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GPGGGAPR 11
|||||
DB 214 GPGGGHPR 221

RESULT 11
US-11-143-980-34
; Sequence 34, Application US/11143980
; Publication No. US20050272133A1
; GENERAL INFORMATION:
; APPLICANT: Hucul, John
; APPLICANT: Haltli, Bradley A.
; APPLICANT: Wagenaar, Melissa M.
; APPLICANT: Graziani, Edmund
; APPLICANT: Summers, Mia
; APPLICANT: Kulowski, Kerry
; APPLICANT: Pong, Kevin
; TITLE OF INVENTION: Biosynthetic Gene Cluster for the Production of a Complex
; TITLE OF INVENTION: Polyketide
; FILE REFERENCE: AM-101426US
; CURRENT APPLICATION NUMBER: US/11/143,980
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/664,483
; PRIOR FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: US 60/576,895
; PRIOR FILING DATE: 2004-06-03
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Streptomyces sp.
US-11-143-980-34

Query Match 67.5%; Score 40.5; DB 7; Length 280;
Best Local Similarity 75.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 RASGPGG-GAPR 11
|||||
DB 116 RPSGPGGGGPR 127

RESULT 12

US-11-096-568A-26217
; Sequence 26217, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26217
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(558)
; OTHER INFORMATION: Ceres Seq. ID no. 13498878
US-11-096-568A-26217

Query Match 66.7%; Score 40; DB 7; Length 558;
Best Local Similarity 63.6%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RASGPGGGAPR 11
|||||
DB 390 RQEGPAGGPR 400

RESULT 13

US-10-531-036-35
; Sequence 35, Application US/10531036
; Publication No. US20060015951A1
; GENERAL INFORMATION:
; APPLICANT: Eulenber, Karsten
; APPLICANT: Meise, Martin
; APPLICANT: Molitor, Andreas
; APPLICANT: Steuernagel, Arnd
; TITLE OF INVENTION: Proteins Involved in the Regulation of Energy Homeostasis
; FILE REFERENCE: 2923-696
; CURRENT APPLICATION NUMBER: US/10/531,036
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: PCT/EP03/11352
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: EP 02024747.4
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: EP 02023560.2
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: EP 02022880.5
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-531-036-35

Query Match 66.7%; Score 40; DB 6; Length 974;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 RASG--PGGGAP 10
|||||
DB 6 RAGGPPPGGGAP 17

RESULT 14
US-11-087-099-7762
; Sequence 7762, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:

; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 7762
; LENGTH: 1832
; TYPE: PRT
; ORGANISM: Podospora anserina
US-11-087-099-7762

Query Match 66.7%; Score 40; DB 7; Length 1832;
Best Local Similarity 77.8%; Pred. No. 3.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 SGFGGGAPR 11
|||
Db 1051 SGSGGGSPPR 1059

RESULT 15

US-11-072-512-2722
; Sequence 2722, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2722
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2722

Query Match 65.0%; Score 39; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGFGGGA 9
|||
Db 56 SGFGGGA 62

Search completed: March 13, 2006, 20:03:31
Job time : 7.50588 secs

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